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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen	in search, using sw model	January 18, 2005, 11:04:00 ; Search (without 62.932 M	US-09-487-790A-1 116 1 KGSWYSMRKMSWKIRPFPQQ 21	BLOSUM62 Gapop 10.0 , Gapext 0.5	1825181 segs, 575374646 residues	hits satisfying chosen parameters:	length: 0 length: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 65 summaries	<pre>UniProt_02:* uniprot_sprot:* uniprot_trembl:*</pre>	the number of results predicted by chance if than or equal to the score of the result ed by analysis of the total score distribut	SUMMARIES	ery tch Lengi	491	7.4 481 2	8.8 468	3.3 485 2	3.3 485 2 1.6 477 1	0.7 321	7 399 2	.7 453 1	.0 270 2 .0 316 2	.0 435 2	.3 312 1	8.3 312 8.3 312	8.3 314 2 8.3 314 2	3 314 2	8.3	346 2	4.0 438 1 FIBG_XENLA 4.0 866 1 FIBA_HUMAN	
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MEDLINE-843305751; PubMed-6383194;
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MEDLINE=97472408; Pubmed=9333233;
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J. Clin. Invest
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=YOB/N. TISSUE-Liver;

A KLAINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altechul S.F., Zeebberg B., Buerow K.H., Schaefer C.F., Bhar N.K.,

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RA Altechnoko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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Robert S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Robert S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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Ritching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RAZWINIARI M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

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R. "Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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MEDLINE=Sprague-Dawley, TISSUE-Liver;
MEDLINE=95143386; PubMed=7841303;
Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.,
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                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.4%; Score 113; DB 2; Length 481; 95.2%; Pred. No. 9.9e-10; ive 1; Mismatches 0; Indels
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STRAINEFUBN; TISSUE=Liver;
Strainsherg (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011715; AAH31715.1; -.
HSSP; P02675; IFZE.
MGD; MGI:99501; Pgb.
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481 AA; 54752 MW; 9902830CF708A155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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Pfam; PF00147; Fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMA
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nes 20; Conservative
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  musculus (Mouse)
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                                                                     NCBI_TaxID=10090;
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Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primatee; Catarrhini; Hominidae; Pan.
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Lounes K.C., Lefkowitz J.B., Henschen-Edman A.H., Coates A.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 491;
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Pred. No. 5e-11;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rupert J.L., Hochachka P.W.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF200356; AAF6619.1; -. InterPro; IPR002181; Fibrinogen_C. Pfam; PF00147; Fibrinogen_C. 1. NON TER 1 SEQUENCE 30 AA; 3709 MW; 89105BDC9C4FCB89 CRC64;
                                                                                                                                                                                                                                         VARIANTS CONGENITAL AFIBRINOGENEMIA ARG-383 AND ASP-430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Fibrinogen, B beta polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 116; DB 1; 100.0%; Pred. No. 3.3e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                      human genes.";
c. Genet. 22:231-238(1999).
                                                                                                                                                                                            Genet. 23:373-373(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.4%;
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Best Local Similarity 95.29
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Local Si...
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Q9N1E1;
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                                                                                                                                                                                                                                                                                               -i- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                 STRAIN=Wistar, TISSUE=Liver;
MEDLINE=87134033; PubMed=3817019;
Sobczak J., Lotti A.-M., Taroux P., Duguet M.;
Molecular cloning of mRNA sequences transiently induced during rat liver regeneration.";
Exp. Cell Res. 169:47-56(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00186; FBG; 1. --
PROSITE; PS00514; FIBRIN AG C_DOMAIN; 1.
Blood coagulation; Direct protein sequencing; Glycoprotein; Plasma;
                                                                                                                                                                        chain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inked (GlcNAc. . .) (Potential)
-> ILS (in Ref. 3).
SEQUENCE OF 1-26 FROM N.A.
SEQUENCE OF 1-26 FROM N.A.
MEDLINE=84194000; PubMed=6232608;
FOWLKSE D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
FOUCHIAL basis for regulation of the coordinately expressed fibrinogen genes: homology in the 5' flanking regions.";
Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fibrinopeptide B.
Interchain (with alpha chain)
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interchain (with gamma chain)
                                                                                                                                    SEQUENCE OF 183-479 FROM N.A.
MEDLINE=89778771; PubMed=2673932;
Bastman B.M., Gilula N.B.;
"Cloning and characterization of a cDNA for the B beta cha fibrinogen: evolutionary conservation of translated and 3' untranslated sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fibrinogen beta chain.
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By similarity.
By similarity.
N-linked (GlcNAcLSI -> ILS (in R
                                                                                  SEQUENCE OF 19-12.
Blomback B., Blomback M., Grondahl N.J.;
"Studies on fibrinopeptides from mammals.";
Acta Chem. Scand. 19:1789-1791(1965).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U05675; AAA64866.1; --
EMBL, M37220; AAA41160.1; --
EMBL, K01336; AAA41150.1; --
EMBL, M35602; AAA41159.1; --
PIR; A05299; A05299.
PIR; 167595; 167595.
HSSP, P02675; 1FZE.
RGD; 2604; Fgb.
InterPro; IPR002181; Fibrinogen_C.
PFAM: PF00147; Fibrinogen_C.
                                                                                                                                                                                                                         SEQUENCE OF 425-479 FROM N.A.
                                                                                                                                                                                                    Gene 79:151-158 (1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eggregation.
-!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds.
-!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot. The soft clot is converted into the hard clot by factor XIIIA which catalyzes the epsilon-(gamma-glutemyllysine cross-linking between gamma chains (stronger) and between alpha chains (weaker) of different
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Martinelli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,
Hurrell J.G.R., Leach S.J., Scheraga H.A.;
"Amino acid sequences of portions of the alpha and beta chains of
bovine fibrinogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibrinogen.";
Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).
-!- FUNCTION: Fibrinogen has a double function: yielding monomes
polymerize into fibrin and acting as a cofactor in platelet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2004 (Rel. 45, Last annotation update)
Fibrinogen beta chain precursor (Contains: Fibrinopeptide B)
                                                                                                                                                                                                                                                                                                                                 Score 106; DB 1; Length 479;
Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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Sjoquist J., Blomback B., Wallen P.;
Ramino acid Sequence of bovine fibrinopeptides.";
Ark. Kemi 16:425-436(1960).
L -> Q (in Ref. 5).
S -> T (in Ref. 5).
S -> A (in Ref. 5).
R -> K (in Ref. 5).
V -> F (in Ref. 5).
WW, ECGCGDB77C3E0ECO CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 KGSWYSMRRMSMKIRPVFPQQ 479
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01-FEB-1996 (Rel. 33, Last seq
                                                                                                                                                                                                                                                                                                                                      91.48;
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                                                                                                                                                                                                                                          479 AA;
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FIBB_BOVIN
ID FIBB_BOVIN
$\text{POS}^{0.0} \text{Color}^{0.0} \text{Color}^{0.0}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cleavage site.";
Biochemistry 30:3290-3294(1991).
-!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
MEDLINE=91182745; PubMed=2009266;
Weissbach L., Oddoux C., Procyk R., Grieninger G.;
"The beta chain of chicken fibrinogen contains an atypical thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                By similarity.
By similarity.
By similarity.
N-linked (GlcNAc. . .) (Probable)
                                                                                                                                                                                                                      Fibrinopeptide B.
Pibrinogen beta chain.
Pyrolidone carboxylic acid.
Sulfctyrosine.
Cleavage (by thrombin, release
fibrinopeptide B).
                                                                                                                                                                  PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
3D-structure; Blood coagulation; Direct protein sequencing; Glycoprotein; Plasma; Platelet; Pyrrolidone carboxylic acid; Sulfation.

1 21 Fibrinopeptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.8%; Score 103; DB 1; Length 46
81.0%; Pred. No. 4.1e-08;
ive 4; Mismatches 0; Indela
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Interchain (with alpha).
Interchain (with gamma).
Interchain (with gamma).
Interchain (with gamma).
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                                                                            EMBL; V00110; CAA23444.1; -.. PDB; 1DEQ; X-ray; B/FO/Pee1-468. PDB; L3Y2; X-ray; O/R=61-116. PDB; L3Y3; X-ray; O/R=61-116. Interpro; IPR002181; Fibrinogen_C. Pfam; PP00147; Fibrinogen_C. SMART; SM00186; FBG; 1.
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-!- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds.
-!- PTM: Conversion of fibrinopen to fibrin is triggered by thrombin, which cleaves fibrinopetides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot. The soft clot is converted into the hard clot by factor XIIIA which catalyzes the epsilon-(gamma-glutamyl) lyabhe cross-linking between gamma chains (stronger) and between alpha chains (weaker) of different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
similarity).
similarity).
similarity).
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Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-linked (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cleavage (by thrombin; release fibrinopeptide B)
Interchain (with alpha) (By simi. Interchain (with alpha) (By simi. Interchain (with gamma) (By simi. Interchain (with alpha) (By simi. Interchain (with gamma) (By simi.) Interchain (with gamma) (By simi.)
                                                                                                                                                                                                                                                                                                                          PIR, A38463; A38465.

PDB; 1BI3; X-ray; B/E=1-463.

PDB; 1MIJ; X-ray; B/E=1-463.

PDB; 1MIJ; X-ray; B/E=1-463.

PDB; 1MIJ; X-ray; B/E=1-463.

PEam; PF00147; Fibrinogen_C; 1.

SWART; SW00186; PBC; 1.

3D-8tructure; Blood coagulation; Direct protein sequencing; Glycoprotein; Plasma; Platelet; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fibrinogen beta chain.
Sulfotyrosine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 97; DB 1; Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                        SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fibrinopeptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
By similarity.
By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KGSWYSMRKMSMKIRPFFP 19
                                                                                                                                                                                                                                                                                                                 EMBL; M58514; AAA48770.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Conservative
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80
84
197
201
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TISSUE=Kidney;
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NON TER
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DISULFID
DISULFID
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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      Richard R. L., Feingold E. A., Grouse L. H., Derge J. G.,
Klausner R. D., Collins F. S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S. P., Zeeberg B., Buetow K. H., Schaefer C. F., Bahat N. K.,
Hopkins R. F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M. B., Bonaldo M. F., Carannori P., Prange C.,
Brownstein M.J., Usdin T. B., Tochhyuki S., Carnnori P., Prange C.,
Raha S. S., Loquellano N. A., Peters G. J., Abramson R. D., Mullahy S. J.,
Richards S., Worley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W.,
Villalon D. K., Muzny D. M., Sodergren E. J., Lu X., Glbbs R. A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G. G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G. G.,
Blakesley R. W., Touchman J. W., Green E. D., Dickson M. C.,
Jones A. C., Grimwood J., Schmutz J., Myers R. M., Butterfield Y. S.,
Jones S. J., Marra M. A.,
T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            **MEDLINE=22388257; PubMed=12477932;

**REDLINE=22388257; PubMed=12477932;

**Retausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

**Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

**Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

**Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

**Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

**Rapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

**Raha S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunaratne P.H.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gaby E.J., Hulyk S.W.,

**Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**Villalon D.K., Wuzny D.M., Madan A., Rodrigues S., Sanchez A.,

**Mhiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.3%; Score 85; DB 2; Length 485
66.7%; Pred. No. 3.7e-05;
Viemarches 2; Indels
                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC066629, AAH66629.1;
InterPro; IPR02181; Fibrinogen_C.
Pfam; PP0047; Fibrinogen_C;
SMART; SM00186; FBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 485 AA; 54407 MW; A362250444BBOFF3 CRC64;
                                                                                                                                                                                                                                                                               and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KGSWYSMRKMSMKIRPFFPQQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-2004 (TrEMBLrel. 27, 24-MAY-2004 (TrEMBLrel. 27, 24-MAY-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 66.7 tes 14; Conservative
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skallska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 37-477 FROM N.A.

**MEDILIBE-87076582; PubMed=3790537;

**MEDILIBE-87076582; PubMed=3790537;

**ROMINES V.L., Doolittle R.F., Pontes M., Strong D.D.;

"Complementary DNA sequence of lamprey fibrinogen beta chain.";

Biochemistry 25:6512-6516(1986).

-!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aggregation.

Subunir: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds. PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot. The soft clot is converted into the hard clot by factor XIIIA which cacalyzes the epsilon-(gamma-glutamy)lysine cross-linking between gamma chains (stronger) and between alpha chains (weaker) of different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-36. PubMed=999898; MEDLINE=77065679; PubMed=999898; Cottrell B.A., Doolittle R.F.; "Amino acid sequences of lamprey fibrinopeptides A and B and characterizations of the junctions split by lamprey and mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
1-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Pibrinogen beta chain (Contains: Pibrinopeptide B] (Fragments).
Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.3%; Score 85; DB 2; Length 485; Best Local Similarity 66.7%; Pred. No. 3.7e-05; Matches 14; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 1 fibrinogen C-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54407 MW; A3622504448B0FF3 CRC64;
                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 KGSWYSLKTISMKIRPYFKQK 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KGSWYSMRKMSMKIRPFFPQQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, BC06629, AAH6629.1,
Hypothetical protein.
SEQUENCE 485 AA, 54407 MW
                                                                                                                                                                                                                  cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Kidney;
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420
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463
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477 AA;
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TISSUE=Whole;
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                                                                                                                                                                                                                                                                                                                                                rissum=Whole;
                                              STRAND
STRAND
SEQUENCE
                                                                                             459
                                                                                                                         Q7SYN8;
STRAND
STRAND
TURN
TURN
STRAND
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STRAND
HELIX
                                                                                                                    Q7SYN8
                                                                                                            RESULT 10
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                                                                                                                     8
                                                                                        (B
                                                      Fibrinogen beta chain.
Sulfocyrosine.
N-linked (GlCNAc. . ).
Interchain (with alpha chain) (By similarity) interchain (with alpha chain) (By similarity).
Interchain (with gamma chain) (By linterchain) (with gamma chain) (By linterchain) (with gamma chain) (By
    PDB; 1LWU; X-ray; B/E/H/K=155-477.
PDB; 1N73; X-ray; B/E=155-477.
InterPro; 1PR002181; Fibrinogen_C.
SMART; SM00186; FBG; 1.
PROSITE; PS00514; FIBRIN_AG C_DOMAIN; 1.
3D-efructure; Blood coagulation; Direct protein sequencing; Glycoprotein; Plasma; Sulfation.
PEPTIDE
                                                                                                        sımılarıty)
Interchain (with gamma chain)
                                                                                                 chain)
                                                                                            similarity).
Interchain (with alpha
                                                                                                               similarity).
By similarity.
By similarity.
By similarity.
                                                                                                      similarity)
                                              36
37
477
13
27
84
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3323
3333
3347
3354
3356
3358
373
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297
307
                                                   36
137
27
27
84
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                                                                                                           216
                                                                                                                   DISULPID
DISULPID
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HELIX
HELIX
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HELIX
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STRAND
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CHAIN
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DISULFID
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HELIX
TURN
TURN
STRAND
TURN
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MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itachul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Altschul S.F., Zeeberg B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Consider M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Robard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nichards B., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.B.,

Jones J.G., J.J., J
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Name=LOC397825;

Name=Loc3
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MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
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                                                                                                                                 Score 83; DB 1; Length 477;
Pred. No. 7.7e-05;
4; Mismatches 1; Indels
54270 MW; B8A95E7E32D09D18 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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Best Local Similarity 73.7%;
Matches 14; Conservative
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Gaps

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Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A.;
                                                               TISSUE=Liver;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Bloecker H., Boecher M., Wiemann S.;
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2013) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538098; CAD98014.1; -.
InterPro; IPR0012H1; Fibrinogen C.
Ffam; PF00147; Fibrinogen C.;
SWART; SW00186; FBG; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                  51.7%; Score 60; DB 2; Length 399; 64.7%; Pred. No. 0.36;
   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                  4; Indels
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SEQUENCE 437 AA; 49496 MW; 3D73A7BC1E71381B CRC64;
                                                                                                                                                                                                                                                  SEQUENCE 399 AA; 45092 MW; 9451321C29AB5C9A CRC64;
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Homo sapiens (Human).
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nes 11; Conservative
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                                                 SEQUENCE FROM N.A.
                    NCBI_TaxID=9606;
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"CDNA and amino-acid sequences and organization of the gene encoding
"CDNA and amino-acid sequences and organization of the gene encoding
the B beta subunit of fibrinogen from Xenopus laevis.";
Gene 160:223-228(1995).
BMB., 1016618, AAA85283.1; -.
HSSP; P02675; LITJ.
InterPro: IPR002181; Fibrinogen_C.
Pfam: PF00147; Fibrinogen_C;
SMART; SM00186; FBG; 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                     Length 321;
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                                                                                                                                                                / Match 70.7%; Score 82; DB 2; Length 321
Local Similarity 77.8%; Pred. No. 7.3e-05;
Nes 14; Conservative 3; Mismatches 1; Indels
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Klein S., Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; BC054126; AAH54126.1; -.
Interpro; IRR001181; Fibrinogen_C.
Pfam; PF00147; Fibrinogen_C: 1.
SWART; SM00186; FBG; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 B fibrinopeptide.
488 fibrinogen B-beta subunit.
54803 MW; 660E03844BBC6414 CRC64;
                                                                                                                                 SEQUENCE 321 AA; 36519 MW; E0C41FCC3EB40DEF CRC64;
                                                                                                                                                                                                                                                                                                                                                               Q91589; Q91546;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Fibrinogen B-beta subunit precursor.
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                                                                                                                                                                                                                                                       303 KDSWYSMKKMSIKIRPYF 320
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Best Local Similarity
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gamma-fibrinogen.";
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 CTISSUE—Skeletal muscle;

XX STGUENCE FROW N.M. (120) FUND GARDANATA, N. (120) FUND GARDANATA, N. (120) FUND GARDANATA, N. (120) FUND GARDANATA, N. (120) FUND GARDANATA, STRUBBERS, N. (120) FEINGOIG E.A., Grouse L.H., Derge J.G., Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Nordan H., Moore T., Max S.I., Wang J., Heich F., Dordan H., Moore T., Max S.I., Wang J., Heich F., Dordan H., Moore T., Max S.I., Wang J., Haich F., Dordan H., Moore T., Max S.I., Wang J., Haich F., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Andramson R.D., Mullahy S.J., Robat S.A., McEwan P.J., McKernan K.J., Malek J.A., Gauratane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Andran J.W., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rollwood J., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A., Rotton D.E., Andrewson M. Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Rotton Human D.M., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Fander S.M., Andrewson M.D., Schein J.E., Jones S.J.M., Marra M.A., Fander S.M., Andrewson M.C., Schein J.E., Jones S.J.M., Marra M.A., Fander S.M., Andrewson M.C., Schein J.E., Jones S.J.M., Marra M.A., Fander S.M., Andrewson M.C., Schein J.E., Jones S.J.M., Marra M.A., Fander S.M., Andrewson M.C., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Marra M.A., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Marra M.A., Schein J.E., Jones S.J.M., Marra M
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                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional prediction of the coding sequences of 33 new genes deduced by analysis of cDNA clones from human fetal liver."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                          MEDLINE-83283434; PubMed-6688357;
Chung D.W., Chan W.-Y., Davie B.W.;
"Characterization of a complementary deoxyribonucleic acid coding for
the gamma chain of human fibrinogen.";
                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Fetal liver;
Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Henschen A., Lottspeich F., Southan C., Topfer-Petersen E., "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B).
Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Foel C.L., Yi
Nickerson D.A.;
"SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).",
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
Pergamon Press, Oxford (1980).
               Rixon M.W., Chung D.W., Davie E.W.; "Nucleotide sequence of the gene for the gamma chain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 285-437 FROM N.A. (ISOFORMS GAMMA-A AND GAMMA-B) MEDLINE-85030379; PubMed=6092346; Fornace A.J. Jr., Cummings D.E., Comeau C.M., Kant J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92119334; PubMed=1685103;
Marchetti L., Zanelli T., Malcovati M., Tenchini M.L.;
"Polymorphism of the human gamma chain fibrinogen gene.";
DNA Seq. 1:419-422(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISOFORM GAMMA-A).
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM GAMMA-A)
MEDLINE=85252774; PubMed=2990550;
                                                                    Biochemistry 24:2077-2086(1985).
                                                                                                                                                                                                     Biochemistry 22:3250-3256(1983)
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Henschen A., Lottsp
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                                                       fibrinogen.
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Cottrell B.A.,
                                                                                                       MEDINE=84069777; PubMed=6689067;
Imam A.M.A., Eaton M.A.W., Williamson R., Humphries S.;
"Isolation and characterisation of CDNA clones for the A alpha- and
                                                                                                                                                                                                                                                                                                                                                                                                                                  of a human fibrinogen gamma-
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gamma' chain.";
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Horvitz B.H., Varadi A., Scheraga H.A.;
"Localization of a fibrin gamma-chain polymerization site within segment Thr-374 to Glu-396 of human fibrinogen.";
Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984 (1984).
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Pergamon Press, New York (1978).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLATELET AGGREGATION SITE.
MEDLINE-84203545; PubMed-6326808;
Kloczewiak M., Timmons S., Lukas T.J., Hawiger J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-83254370; PubMed-6575689;
Henschen A., Loctspetch F., Kehl M., Southan C.;
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                                                                                                                                                                                                                   gamma-chains of human fibrinogen.";
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Doolittle R.F.;
"Fibrinogen and fibrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chain variant (gamma').";
Biochemistry 20:6146-6149(1981).
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                                                                          SEQUENCE OF 209-270 FROM N.A
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les 10; Conservative
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Pratt K.P., Cote H.C.F., Chung D.W., Stenkamp R.E., Davie B.W.;
Pratt K.P., Cote H.C.F., Chung D.W., Stenkamp R.E., Davie B.W.;
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=45438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cai Q., Storey K.B.;
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EMBL; U44829; AAA97879.1;
InterPro; IPR002181; Fibrinogen_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.

MEDLINES-97169449; PubMed-29016719;
Yee V.C., Pratt K.P., Cote H.C.F., 1e Trong I., Chung D.W.,
Davie E.W., Stenkamp R.E., Teller D.C.;
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Structure 5:125-138(1997).
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                                                                                                                                                                  Ginsberg M.H.; with a common
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MEDLINE=81054908; Pubmed=6933547;
Wolfenstein-Todel C., Mosesson M.W.;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Fibrinogen gamma subunit (Fragment).
Rana sylvatica (Wood frog).
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                                                                                                                                     MEDLINE=84185664; PubMed=6325435;
Plow B.F., Srouji A.H., Meyer D., Marguerie G.,
"Evidence that Urree adhesive proteins interact
recognition site on activated platelets.";
J Biol. Chem. 259:5388-5391(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.7%; Score 60; DB 1;
64.7%; Pred. No. 0.41;
tive 2; Mismatches
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01-NOV-1996 (TrEMBLrel. 01, Created)
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Matches 11; Conservative
                                                                                                                    PLATELET AGGREGATION SITE
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  RAT REPRESENT RE
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MEDLINE=96144287; PubMed=8566791;
Simpson-Haidaris P.J., Wright T.W., Barnest B.J., Hui Z., Neroni L.A.,
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
10-MAR-2004 (TrEMBLrel. 26, Last annotation update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
12-MARSTAL STATE (Tragment)
13-MARSTAL DELOCATION (European polecat)
14-MARMANTAL MELAZOA; Chordata; Craniata; Vertebrata; Euteleostomi;
14-MARMANTAL MARMANTAL CARNIVORA; Fissipedia; Mustelidae; Mustelinae;
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                                                                                                                                                             Score 58; DB 2; Length 270;
Pred. No. 0.5;
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STRAIN=White Leghorn; TISSUE=Liver;
Gao Y., Weissbach L., Fu Y., Grieninger G.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF087432; AAC36476.1; -.
Pfam; PF00147; Fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
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SRQUENCE 270 AA; 30878 MW; A780763F14288CFC CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Gene 167:273-278(1995).
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InterPro; IPR002181; Fibrinogen_C.
InterPro; IPR009053; Prefoldin.
Pfam; PF00147; Fibrinogen_C; 1.
SWART; SM00186; PBG; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
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activity.
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SEQUENCE FROM N.A.

STRAIN=FVB/N. TISSUE=Liver, and Salivary gland;

MEDLINE=2388257, PubMed=12477932;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Radschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhate N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,

A Strapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,

A Rapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Broak S.A., McEwan P.J., McKernan K.J., Make J.A., Gunzatne P.H.,

Radar S., Worley K.C., Hale S., Garcia A.M., Gaty L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaty L.J., Hulyk S.W.,

Radan A., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Schwutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

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                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                          Score 58; DB 2; Length 435;
Pred. No. 0.84;
                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0199506; AAH19506.1; -.
EMBL; BC0199539; AAH19828.1; -.
HSSP; P02679; 1FZF.
                                                                                                                                                                                                                                       27 435 fibrinogen gamma chain.
435 AA; 49642 MW; 91D2BC7FE86E0766 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:95526; Fgg.
InterPro; IPR002181; Fibrinogen_C.
Pfam, PF00147; Fibrinogen_C; 1.
SWART: SW00186; FBG; 1.
PROSITE; PS00514; FIBRIN AG C_DOMAIN; 1.
SEQUENCE 436 AA; 4939I MW; FF45A3486C92143E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBVCM7; QBWUR3;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Liver, and Salivary gland;
PDB; 1E13; X-ray; C/F=27-435.
PDB; 1M1J; X-ray; C/F=27-435.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPRO02181; Fibrinogen C.
Pfam; PPO0147; Pibrinogen C;
SMART; SM00186; FBG; 1.
PROSITE; PS00184; FIBRIN AG C_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436 AA.
                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                      Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibrinogen, gamma polypeptide.
                                                                                                                                                                                                                                                                                                               50.0%;
                                                                                                                                                                                                                                                                                                                                    71.48;
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402 WYSMKKTTMKIIPF 415
                                                                                                                                                                                                                                                                                                                                                                                                        4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                               SEQUENCE
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SEQUENCE 1
                                                                                                                                                                                              Signal.
SIGNAL
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Q8VCM7
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MEDINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899;
X MEDINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899;
X Krausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
X Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jedan H., Moore T., Max S.I., Wang J., Heish F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheefer T.B.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
A Generation and initial analysis of more than 15,000 full-length human
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93290661; PubMed-8390249;
Yamamoro T., Gotoh M., Saeaki H., Terada M., Kitajima M.,
Hivohashi S.;
"Molecular cloning and initial characterization of a novel fibrinogen-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21363035; PubMed=11470158; DOI=10.1016/S0167-4781(01)00249-4; Hara H.; Voshimura H.; Uchida S., Toyoda Y., Aoki M., Sakai Y., Morimoto S., Shiokawa K.; Morimoto S., Shiokawa K.; Molecular cloning and functional expression analysis of a cDNA for
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human hepassocin, a liver-specific protein with hepatocyte mitogenic
                                                                                                                                                                                                                                                           Q08830; Q96KW6; Q96QM6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Fibrinogen-like protein 1 precursor (Hepatocyte-derived fibrinogen-related protein 1) (HFREP-1) (Hepassocin) (HP-041).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Length 436
                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- TISSUE SPECIFICITY: Liver specific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- FUNCTION: Has hepatocyte mitogenic activity.
-!- SUBUNIT: Homodimer (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related gene, HFREP-1.";
Biochem. Biophys. Res. Commun. 193:681-687(1993).
DB 2;
50.0%; Score 58; DB 2; 58.8%; Pred. No. 0.84;
                                                                                                                                                                                                                                           312 AA
                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1520:45-53(2001).
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                                         3,
                                                                                                              | ||||:::||| ||
398 KSRWYSMKETTMKIIPF 414
                                                                                     17
                                                                                                                                                                                                                                                                                                                                                                                                 Name=FGL1; Synonyms=HFREP1;
                                                                                     1 KGSWYSMRKMSMKIRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences."
                                         10; Conservative
                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
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290 GWWYSLKSVVMKIRPNDFIP 309
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Best Local Similarity 55.0%
                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      Fibrinogen-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                       AAP35281;
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Q71KU9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 22
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                                                                                                                                                AAP35281
AAP35281
AAP35281
AAP370 AAP
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 48.3%; Score 56; DB 1; Length 312; Local Similarity 55.0%; Pred. No. 1.2; es 11; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
By similarity.
By similarity.
I - 7 (in Ref. 1).
I - > V (in Ref. 1).
F - > L (in Ref. 2).
W, 26BC82124E6660C2 CRC64;
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EMBL, PA1689913, AAM88911.1; -.
HSPP, P02671; 1FZD.
InterPro; IPR002181; Fibrinogen_C.
FFam; PF00147; Fibrinogen_C; 1.
SWART; SM00186; FGB; 19
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SEQUENCE 312 AA; 36377 WW; 7330F3D55A0BD619 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fibrinogen-like protein 1. Fibrinogen C-terminal. Interchain (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 605776; ...
GO; GO:0005577; C:fibrinogen complex; TAS.
HICEPRO; IPR002181; Fibrinogen C.
Pfam; PF00147; Fibrinogen C; 1.
SMART; SM00186; FBG; L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00514; FIBRIN AG C_DOMAIN; 1.
Direct protein sequencing; Signal.
SIGNAL 1 22
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                                                                                                                                                                                                                                  EMBL; D14446; BAA03336.1; -. EMBL; D87342; BAB70690.1; -.
                                                                                                                                                                                                                                                                                        EMBL; BC007047; AAH07047.1;
PIR; JN0596; JN0596.
HSSP; P02671; 1FZD.
Genew; HGNC:3695; FGL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248
15
69
72
105
312 AA;
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Best Local Similarity
Matches 11; Conserv
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TISSUE=Liver;
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DISULFID
DISULFID
CONFLICT
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08NG32;
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      요
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2 GSWYSMRKMSMKIRP--FFP 19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
Phelan M., Farmer A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name-Mirel;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                             Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator(TM) System Donor
                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 48.3%; Score 56; DB 2; Length 312; 1 Similarity 55.0%; Pred. No. 1.2; 11; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.3%; Score 56; DB 2; Length 314; 55.0%; Pred. No. 1.3; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Liver;
STRAIN=C57BL/6J; TISSUE=Liver;
Submitted (JAN-2002) to the Jo., Li Y., Liu H., Xu Y.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF478470; AAQ05798.1; --
InterPro; IPR002181; Fibrinogen_C.
InterPro; IPR00181; Fibrinogen_C.
SMART; SM00184; FIBRIN AG C. DOMAIN; 1.
SRART; SR00184; FIBRIN AG C. DOMAIN; 1.
SRQUENCE 314 AA; 36438 MW; 61795498265E76B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BT006635; AAP35281.1; -.
SEQUENCE 312 AA; 36379 MW; 9297153AEA746C31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
  Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 GWWYSLKSVVMKIRPNDFIP 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 GWWYSLKSVVMKIRPSDFIP 311
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02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovinae; Bos.
NCBI_TaxID=9913;
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                                                                                                                                   Query Match
                                                                                                                                                                  Matches
     SERFFS
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                                                                                                                                                                                                                                                                                                                                    REQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TRAIN=FVB/N, TISSUE=Liver;

RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Straubberg R.D., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Andechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Booker M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheefer T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Male S., Garcia A.N., Gay L.J., Hulyk S.W.,

Richards S., Worley V.C., Hale S., Garcia A.N., Gay L.J., Hulyk S.W.,

Richards S., Worley N.M., Sodergren B.J., Lu X., Gibbs R.A.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley W. S., Shevchenko Y., Bouffard G.G.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

R Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R Generation and initial analysis of more than 15,000 full-length human and marsh A. Maring M. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56; DB 2; Length 314;
Pred. No. 1.3;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Liver;
Strausberg R.;
Submitred (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021946; AAH21946.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:102795; Fgll.
InterPro; IPR002181; Fibrinogen_C.
Pfam; PF00147; Fibrinogen_C; 1.
PR00145; FBG; 1.
PROSTE; PS00514; FTBRIN AG C DOMAIN; 1.
SEQUENCE 314 AA; 36439 MW; 52C16CA9C2D0386A CRC64;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Fibrinogen-like protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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STRAIN=C57BL/6J; TISSUE=Liver;
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55.0%;
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nes 11; Conservative
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                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                               NCBI_TaxID=10090;
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02-MAR-2004 (
02-MAR-2004 (
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensealsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 25-63.
MEDLINE=77112616; PubMed=836881;
Tippl R., Fietzek P.P., Wachter E., van Delden V.;
"Disulfide-linked cyanogen bromide peptides of bovine fibrinogen. I Isolation and sequence analysis of the chain constituents from the
           i Y., Liu H., Xu Y.;
a novel mouse liver-specific gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89366676; PubMed=2771651;
Brown W.M., Dziegielewska K.M., Foreman R.C., Saunders N.R.;
"Nucleotide and deduced amino acid sequence of a gamma subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochim. Biophys. Acta 490:420-429(1977).
-1- FUNCTION: Fibrinogen has a double function: yielding monome: polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                               Score 56, DB 2; Length 314;
Pred. No. 1.3;
3; Mismatches 4; Indels
Yan J., Ying H., Gu F., He J., Li Y., Liu H., Xu Y.;
"Cloning and characterization of a novel mouse liver-spec
MFIREI, ortholog to human LFIRE-1, up-regulated in liver
regeneration.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF478470; AAQ05798.1; -.
SEQUENCE 314 AA; 36438 MW; 61795498265E76B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 fibrinogen C-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Fibrinogen gamma-B chain precursor (Gamma').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 17:6397-6397(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | |||:::||||| | | GWWYSLKSVVMKIRPSDFIP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GSWYSMRKMSMKIRP--FFP 19
                                                                                                                                                                                                                                                                                                       48.3%;
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PIR; S05313; S05313.
PDB; 1DEQ; X-ray; C/F=25-436.
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                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino terminal region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bovine fibrinogen."
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds. ALTERNATIVE PRODUCTS:
                                 Event=Alternative splicing; Named isoforms=2;
                                                      IsoId=P02680-1; Sequence=Displayed;
                                            Name=Gamma-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
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MEDIJNE=8194000; PubMed=6232608;

MEDIJNE=8194000; PubMed=6232608;

Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;

Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;

Fowlcantial basis for regulation of the coordinately expressed fibrinogen genes: homology in the 5' flanking regions.";

Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).

-! FUNCTION: Fibrinogen has a double function: yielding monomers that aggregation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                      Gaps
                                 SMART; SMO186; FB2.13.
PROSITE; BS00516; FB1 LAG C DOMAIN; 1.
3D-Structure; Blood coagulation; Calcium; Direct protein sequencing; Glycoprotein; Plasma; Platelet; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-83129318; PubMed=6897622;
Crabtree G.R., Kant J.A.;
"Organization of the rat gamma-fibrinogen gene: alternative mRNA splice patterns produce the gamma A and gamma B (gamma ') chains of fibrinogen.";
                                                                                            Fibrinogen gamma-B chain.
N-linked (GlcNAc. . .) (Probable).
By similarity.
By similarity.
Interchain (with C-33).
Interchain (with Deta).
Interchain (with alpha).
Interchain (with alpha).
Interchain (with alpha).
Interchain (with alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=87174801; PubMed=3562236;
Morgan J.G., Holbrook N.J., Crabtree G.R.;
"Nucleotide sequence of the gamma chain gene of rat fibrinogen:
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                 Length 444;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                             50244 MW; 4573C994DE715C49 CRC64;
                                                                                                                                                                                                                                                                                48.3%; Score 56; DB 1; 62.5%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Fibrinogen gamma chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                    445 AA.
                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved intronic sequences.";
Nucleic Acids Res. 15:2774-2776(1987).
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
PDB; 1JY2; X-ray; P/S=25-72.
PDB; 1JY3; X-ray; P/S=25-72.
InterPro; IPR002181; Fibrinogen_C.
Pfam; PF00147; Fibrinogen_C; 1.
                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                     398 KSRWYSMKKTTMKIIP 413
                                                                                                                                                                                                                                                                                                                          1 KGSWYSMRKMSMKIRP 16
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 31:159-166(1982)
                                                                                                                                                                                                                                                             444 AA;
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                    10;
                                                                                                         CARBOHYD
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                     DISULPID
                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   FIBG RAT
                                                                                                                                                                                                                                      STRAND
HELIX
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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             Incold=P02680-2; Sequence=VSP_001538, VSP_001539;
PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot. The soft clot is converted finto the hard clot by factor XIIIA which catalyzes the epsilon-(gamma-glutemny) lysine cross-linking between gamma chains (stronger) and between alpha chains (weaker) of different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J00733; -; NOT ANNOTATED CDS.

R EMBL; J00734; -; NOT ANNOTATED CDS.

R EMBL; J00735; -; NOT ANNOTATED CDS.

R EMBL; X05860; CAA22289.1; -.

R EMBL; X05860; CAA22289.1; -.

R EMBL; X05861; CAA29289.1; -.

R EMBL; X05861; CAA29289.1; -.

R EMBL; R05879; LFID.

R PIR; A90828; FGRTGA.

R HSSP; P02679; LFID.

R RGD; Z613; FGG

InterPro; 1FR00181; Fibrinogen C.

R Ffam; PF00147; Fibrinogen C.

R SMART; SM00186; FBG; 1.

R SMART; SM00186; FBG; 1.

R Alternative splicing; Blood coagulation; Calcium; Glycoprotein;

W Plasma; Platelet; Signal.
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By similarity.
By similarity.
CE - SDM (in isoform Gamma-A)
/FIId=VSP_001538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fibrinogen gamma chain.
Interchain (with gamma chain)
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Interchain (with gamma chain)
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Pred. No. 1.8;
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                                                                                                                                                                                                                     SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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9D61CCC0168B17A9 CRC64;
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
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399 KTRWYSMKETTMKIIPF 415
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Best Local Similarity 58.8'
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445
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437
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Name=Gamma-A;
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435
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SEQUENCE FROM N.A.
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Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.S.I., Wang J., Hsich F.,
Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunzane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.N., Gapt L.J., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.N., Gapt L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.,
Johns S.J., Marra
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21318995; PubMed=11426320; MEDLINE=21318995; PubMed=11426320; Stover C., Endo Y., Takahadhi M., Lynch N., Constantinescu C., Stover C., Endo Y., Takahadhi M., Hankeln T., Hall R., Gregory S., Fujita T., Schwaeble W., "The human gene for mannan-binding lectin-associated serine protease-2 (MASP-2), the effector component of the lectin route of complement activation, is part of a tightly linked gene cluster on chromosome
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SEQUENCE FROM N.A.
MEDLINE=22867296; PubMed=12975309;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Clark H.F., Gurney A.L., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
                                                                                                                                                                                                                                                                                              TISSUE-Cornea;
MEDLINE=98394383; PubMed=9727400;
Peek R., van Gelderen B.E., Bruinenberg M., Kijlstra A.;
"Molecular cloning of a new angiopoietin-like factor from the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
CDT6 (Angiopoletin-118 factor)
Name-CDT6; ORFNames-UNQ313;
Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota, Metazoa; Ghordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phelan M., Farmer A.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                             Invest. Ophthalmol. Vis. Sci. 39:1782-1788(1998)
                                       346 AA
                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genes Immun. 2:119-127(2001).
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                                       PRELIMINARY;
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                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                        "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";

If choose Res. 13:2265-2270(2003).

REMBL; Y16132; CAA76078.1; -...

REMBL; AJ300188; CAC15271.1; -...

REMBL; BC001881; AAH01881.1; -...

REMBL; BC001881; AAH01881.1; -...

REMBL; BC001881; AAP88804.1; -...

REMBL; BC001881; DAQ88668.1; -...

RESSP; Q9U8WR; 1UC9.

R GO; GO:0006979; P:response to oxidative stress; TAS.

InterPro; IPR00147; Fibrinogen.C.

R PFam; PF00147; Fibrinogen.C.

R PERMS AA; 40018 MW; AECOA601CC498B43 CRC64;
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Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Sebhagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagus A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Номо sapiens (Нимал).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.8%; Score 52; DB 2; Length 346; 60.0%; Pred. No. 6.3; ive 4; Mismatches 2; Indels
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SEQUENCE 346 AA; 40018 MW; AECOA601CC498B43 CRC64;
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Last annotation update)
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Best Local Similarity 60.0
Matches 9; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
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EMBL; J02894; AAA49709.1; -. EMBL; M35548; AAA03247.1; -.
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FIBA HUMAN
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"Isolation and characterization of CDNA clones for the gamma subunit
of Xenopus fibrinogen, the product of a coordinately regulated gene
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93090725; PubMed=1457396; Pt Y. Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J., Roy S.N., Redman C.M., Grieninger G; Roy S.N., Redman C.M., Grieninger G; the human fibrinogen alpha "Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel exon conferring marked homology to beta and gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

BUT, Cao Y., Hertzberg K.M., Grieninger G.;
FU Y., Cao Y., Hertzberg K.M., Grieninger G.;
FI FIDTINGSON Alpha genes: conservation of bipartite transcripts and carboxy-terminal-extended alpha subunits in vertebrates.";
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10-OCT-2003 (Rel. 42, Last annotation update)
Fibrinogen gamma chain precursor.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 235;
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                                                                                  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
101-DEC-2001 (TrEMBLrel. 19, Last annotation update)
101-DEC-3001 alpha-E subunit (Fragment)
101-DEC-3001 Papio (Yellow baboon)
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      235 AA
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                                                          (TrEMBLrel. 01, Created)
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EMBL, U20762; AAA98968.1; -.
InterPro, IPR002181; Fibrinogen_C.
Pfam; PP00147; Fibrinogen_C; 1.
SMART; SM0186; FBG; 1.
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nes 10; Conservative
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   PRELIMINARY;
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01-NOV-1996
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P17634;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeiab-sib.ch).
FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n gamma chain.

n (with C-33) (By similarity).

n (with C-32) (By similarity).

n (with beta) (By similarity).

n (with alpha) (By similarity).

n (with beta) (By similarity).

n (with alpha) (By similarity).
                                                                aggregation.
SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
(alpha, beta and gamma), linked to each other by disulfide bonds.
PIM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot. The soft clot is converted into the hard clot by factor XIIIA which catalyzes the epsilon-(gamma-glutamyl)lysine cross-linking between gamma chains (stronger) and between alpha chains (weaker) of different
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21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Fibrinogen alpha/alpha-E chain precursor [Contains: Fibrinopeptide]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTE; A32670; A32670.
PTR; A32670; A32670.
InterPro; PO2679; ZFIB.
InterPro; PR00181; Fibrinogen_C.
Pfam; PF00147; Fibrinogen_C; 1.
SWART; SW00186; FBG; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
BLood coagulation; Calcium; Glycoprotein; Plasma; Platelet; Signal.
SIGNAL
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MEDILINE=93090725; PubMed=1457396;
Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
Roy S.N., Redman C.M., Grieninger G.;
"Carboxy-terminal-extended variant of the human fibrinogen alpha
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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         Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
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MEDLINE-83283432; PubMed-6688355;
Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
"Characterization of a complementary deoxyribonucleic acid coding for the alpha chain of human fibrinogen.";
Biochemistry 22:3237-3244(1983).
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
"Amino acid sequence studies on the alpha chain of human fibrinogen.
Overlapping sequences providing the complete sequence.";
Biochemistry 18:3410-5416 (1979).
                                                                                                            Chung D.W., Grieninger G.;
"Fibrinogen DNA and protein sequences.";
(In) Ebert R.F. (eds.);
Index of variant human fibrinogens, pp.13-24, CRC Press, Boca Raton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-84069777; PubMed-6689067; Imma A.M., Eaton M.A., Williamson R., Humphries S.; Imma A.M., Eaton M.A., Williamson R., Humphries S.; Impartion and characterisation of CDNA clones for the A alpha- and gamma-chains of human fibrinogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (In) Peeters H. (eds.);Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,Pergamon Press, Oxford (1980).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Henechen A., Lottspeich F., Southan C., Topfer-Petersen E., "Human fibrinogen: sequence, sulfur bridges, glycosylation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=83247396; PubMed=6575389;
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                                          Biochemistry 31:11968-11972(1992).
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MEDLINE=99175089; PubMed=10074346;
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Biochemistry 37:8637-8642(1998)
CROSS-LINKING ACCEPTOR SITES
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GO; GO:0006306; P:DNA methylation; IEA.
GO; GO:0009307; P:DNA restriction; IEA.
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SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
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"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005283; BAC00463.1;
GO; GO:0005284; F:ATP binding; IEA.
GO; GO:0003677; F:NTP-dependent helicase activity; IEA.
GO; GO:0003177; F:NNA binding; IEA.
GO; GO:0008170; F:N-methyltransferase activity; IEA.
GO; GO:0015668; F:type III site-specific deoxyribonuclease ac. . .; IEA.
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Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A.,
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gel formation.";
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141 to serine substitution associated with extra N-glycosylation at A alpha-asparagine-139. Impaired fibrin gel formation but normal fibrin-
facilitated plasminogen activation catalyzed by tissue-type
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Diorio J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,
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Corynabacterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Restriction enzymes type I helicase subunits and related
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;
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                                                 VARIANT KYOTO-2.
MEDLINE=91300048; Pubmed=2070049;
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Biochemistry 38:2941-2946(1999)
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Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M., Burkovski A., Dusch N., Eggeling L., Elkmanns B.J., Galgalat L., Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B., McHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A., Rey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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J. Biotechnol. 104:5-25(2003).
BMBL, BX927157; CAF19007.1; -GO: GO: GO: 0004386; F:helicase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium gluťamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.0%; Score 51; DB 2; Length 1643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00097; CARBAMOYLTRANSFERASE; UNKNOWN_1.
PROSITE; PS00097; NG MTAGE; UNKNOWN_1.
ATP-binding; Helicase; Hydrolase.
SEQUENCE 1646 Aa; 183715 MW; EF060CD1B56248FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1643 AA; 183351 MW; 6AA4C2121894CDE1 CRC64;
InterPro; IFR00610; Asp/Orn_Cotraff.
InterPro; IFR001410; DsAD.
InterPro; IFR001410; DsAD.
InterPro; IFR0012650; Helicase C.
InterPro; IFR0022650; Helicase C.
InterPro; IFR002055; NG Mtase.
InterPro; IFR002051; Ne III.
Interpro; IFR002051; NG MTASE.
Interpro; IFR00092; NG MTASE; UNKNOWN_I.
IFR05ITE; PS00092; NG MTASE; UNKNOWN_I.
INTERPROSITE; NG MTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1297 KISWDSNLKMSLSRGDTFSFDPSSIQMSLYRPFFPQQ 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) DNA or RNA helicase of superfamily II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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Query Match 43.1
Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003
01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STATAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
PubMed=12948626;
Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
Bulkovski A., Dusch N., Eggeling L., Elkmanns B.J., Galgalat L.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
McHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,
Rey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Whole;
MEDLINE-22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamines."; Objection of L-aspartate-derived amino acids and biotechnol. 104:5-25(2003).

EMBL; BX927157; CAF19007.1; -.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                  Length 1646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51; DB 2; Length 1646;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1646 AA; 183715 MW; EF060CD1B56248FF CRC64;
                                                                                                                                                                                                                                                                                                 02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DNA or RNA helicase of superfamily II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1300 KISWDSNLKMSLSRGDTFSFDPSSIQMSLYRPFPPQQ 1336
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                              1300 KIŚWDŚNLKMSLSRGDTFSFDPSSIQMSLYRPFFPQQ 1336
                                                                                                      ------IRPFFPQQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KGSWYSMRKMSMK-----IRPFFPQQ 21
                Score 51; DB 2;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 AA.
                                                                                                                                                                                                                                                              PRT; 1646 AA
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                                                       1; Mismatches
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Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
             44.0%;
37.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.0%;
                                                                                                      1 KGSWYSMRKMSMK----
                                   Best Local Similarity 37.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14, Conservative
                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                                                                                                           CAF19007
CAF19007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tauch A.;
                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Matches
                                                                                                                                                                                                             RESULT 34
CAF19007
ID 02-MA
DT 02-MA
DT 02-MA
DT 02-MA
DE COST
GN COCYT
OC NCD1
COCYT
OC NCD1
RR SEQUE
RR RA RAIT
RR RA
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernen K.J., Malek J.A., Guaratene P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
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Xu C.S., Li W.Q., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,
Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY310161; AAP78769.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Whole;
MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.1%; Score 50; DB 2; Length 439; 50.0%; Pred. No. 17; ive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 2; Length 782;
Pred. No. 32;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
SEQUENCE 782 AA; 86655 MW; 338BC86F2D81DA18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002181; Fibringen_C.
Pfam; PF00147; Fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : ||||: ::||| |
398 RSRWYSMKSVTMKIIP 413
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.
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Best Local Similarity 50.0 Matches 8; Conservative
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Gaps

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TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Length 236;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murakawa M., Freeman M.W.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 9491305; AAL02225.1; -.
MGD; MGI:9501; Fgb.
InterPro; IPR002181; Fibrinogen_C.
Ffam; PF00147; Fibrinogen_C; 1.
SMART; SM00186; FBG; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
   1 1
145 145
145 AA; 16048 MW; 6ABB7C2A8EF3D5A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 AA; 27054 MW; A844F0E40CCB8B01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Fibrinogen B-beta-chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                            42.7%; Score 49.5; DB 2; ilarity 40.9%; Pred. No. 6.3; Conservative 6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49; DB;
Pred. No. 13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                   || || :::|:| |:
61 KGDWYETLQKVSKKLAEHFPNK 82
                                                                                                                                                                                                                                                                                                    1 KGSWY-SMRKMSMKIRPFFPQQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.2%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 88.5
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 KGSWYSMRR 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KGSWYSMRK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                               Local Similarity
tes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGC53392 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
NON TER
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Fqb;
                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q91ZP1
Q91ZP1;
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                                                                                                                                                                                               Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10912P2
10012P2
10012P
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       SHA
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Yu X.-F., Liu W., Chen J., Kong W., Liu B., Zhu Q., Liang F.,
Yu X.-F., Liu W., Chen J., Kong W., Liu B., Zhu Q., Liang F.,
McCutchan F., Piyasirisilp S., Lai S.;
McCutchan F., Piyasirisilp S., Lai S.;
To such an infected with a B/C recombinant and CRF01_AE HIV type 1 in
Southern China.,;
LAIDS Res. Hum. Retroviruses 18:167-170(2002).
EMBL; AY049934; AAL14774.1; ----
CO GO:0019028; C:viral capaid; IEA.
CO; GO:0019039; C:viral envelope; IEA.
CO; GO:001903; C:viral envelope; IEA.
RO; GO:000519; F:structural molecule activity; IEA.
RICEPPRO; IPRO0077; GP120.
REPROSE REPROS
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"Changes in ark..."

Plant Call Physiol. 44:132-136(2003).

Flant Call Physiol. 44:132-136(2003).

EMBL, AF448201; AAL40352.1; -..

GO; GO:0005975; Fishydrolase activity, hydrolyzing O-glycosyl . . ; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR000322; Glyco.hydro.31; 1.

PROSITE; PS00129; GLYCOSYL.HYDROL. F31 1; 1.

PROSITE; PS00707; GLYCOSYL.HYDROL.F31.2; 1.

PROSITE; PS00707; GLYCOSYL.HYDROL.F31.2; 1.

PROSITE; PS00707; GLYCOSYL.HYDROL.F31.2; 1.
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MEDLINE=22497948; bubMed=12610215;
Sanchez M., Gianzo C., Samped J., Revilla G., Zarra I.;
"Changes in alpha-Xylosidase during intact and Auxin-Induced Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pinus pinaster (Maritime pine).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus.
VCBI_TaxID=71647,
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46.7%; Pred. No. 37;
tive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                        910 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 AA
                                                                                  Envelope glycoprotein (Fragment)
                                       1 KGSWYSMRKMSMKIRPFFPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||:: |:|
712 KGSWYNLNDMTMAVK 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KGSWYSMRKMSMKIR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative alpha-xylosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=11676;
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Q901F9;
                                                                                                                                                                                                                                                                                                                                               6VWV8C
                                                                                                                                                                                                                                                                                                        Q8VWV9
                                                                                                                                                                                                                              RESULT 37
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TF20 HUMAN
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X MEDLINE=2257921; PubMed=12693553;

A MEDLINE=22579201; PubMed=12693553;

Okazaki N., Kikuno R., Ohara R., Ingamoto S., Aizawa H., Yuasa S.,

Nakajima D., Nagase T., Ohara R.,

T "Prediction of the coding sequences of mouse homologues of KIAA gene:

TI. The complete nucleocide sequences of 400 mouse KIAA-homologous

CDNAs identified by screening of terminal sequences of cDNA clones

T randomly sampled from size-fractionated libraries.";

MAR Res. 10:35-48(2003).

RE RBL, AK122239; BAC65521.1; -.

RGD, MG:108399; TC£20.

RGD, MG:108399; TC£20.

GO:00003577; F:DNA binding; IEA.

GO: GO:0006355; P:DWA binding; IEA.

RGD, GO:0006355; P:DWA binding; IEA.

R INTERPO: IPRR001965; Zuf_PHD.
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WKIAA0292 protein (Fragment).
Name=Tcf20; Synonyms=mKIAA0292;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                       Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                          "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49; DB 2; Length 343;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         343 AA; 39399 MW; E80A133DF25200CD CRC64;
                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.2%; Scoll 53.3%; Pred. No. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1725 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein S., Strausberg R.; Submitted (14N-2003) to the EMBL/Gen EMBL; BCO44704; AAH44704.1; -. HSSP; Q9UBWB; 1JC9.
InterPro: IPR002181; Fibrinogen_C. Pfam; PF00147; Fibrinogen_C. SWART; SM00186; FBG; 1.
                                                                                                                                                                                                                                                                                         MEDLINE=22341132; PubMed=12454917;
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324 GTTYSLKRVEMKIRP 338
                                                                                                                                                                                                                                                                                                                                                                             Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GSWYSMRKMSMKIRP 16
                                                                                                                                                                                                and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 53.3v
Best Local Similarity 53.3v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo;
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Q80U46
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MEDLINE-20057155; PubMed=10591208; DOI=10.1038/990031;

REDLINE-20057155; PubMed=10591208; DOI=10.1038/990031;

RA DUNHAM I., HURL A.R., COILINS J.E., Bruskiewich R., Beare D.M.,

RA BAGGUING. Mainch J., Ainscough R., Almeida J.P., Babbage A.K.,

RA BAGGUING. Bailey V.E., Colled C., Carter N.P., Barley O.P.,

RA BIT C.P., Blakey S.E., Bridgeman A.M., Buck D., Burges J.,

RA Clegg S.M., Cobley V.E., Colle C.G., Collier R.E., Connor R.,

Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Clegg S.M., Fleming K., French L., Garner A.A.,

RA Gilbert J.G.R. Goward M.B., Grafham D.V., Griffiths M.N.D., Hall C.,

RA Hall R.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

All R.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,

RA Marryn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.

RA Mollips S.H., Plumb R.W., Shuce C.D., Smatley S., Smith M.L.,

ROGIL C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.,

RA Philliams S.H., Plumb R.W., Shuce C.D., Smalley S., Smith M.L.,

RA Soderlund C., Spragon L., Steward C.A., Sulgeron J.E., Swann R.M.,

Vaudin M., Wall M., Wallis S.A., Williams S.A., Walliams S.A., Walliams S.A., Williams S.A., Walliams S.A., Walliams S.A., Walliams S.
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                                                                                                                                                                                                                                                                                                                                O9UGÜO; O14528; Q13078; Q9H4M0;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
pranscription factor 20 (Stromelysin 1 PDGF-responsive element-binding
protein) (SPRE-binding protein) (Nuclear factor SPBP) (AR1).
                                                                                                            Gaps
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MEDLINE=20568288; PubMed=10995766;
Rekdal C., Sjoettem E., Johansen T.;
The nuclear factor SPBP conteains different functional domains and stimulates the activity of various transcriptional activetors.";
J. Biol. Chem. 275:40288-40300(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                            ö
                                                               Length 1725;
                                                                                                          9; Indels
                187463 MW; 4AD460715616E7D6 CRC64;
                                                          Score 49; DB 2; 1
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                PRT; 1960 AA
                                                                                                       1; Mismatches
                                                                                                                                                                                               1475 GKWASYRNMGDLFGPFYPQ 1493
                                                                                                                                                  2 GSWYSMRKMSMKIRPFFPQ 20
                                                          42.2%;
                                                                                                          Conservative
                                   Query Match
Best Local Similarity
9; Conserve
1
1725 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98399843; PubMed=9730594;
Rajadhyaksha A., Riviere M., Van Vooren P., Szpirer J., Szpirer C.,
Rajadhyaksha A., Riviere M., Van Vooren P., Szpirer J., Szpirer C.,
Babin J., Blam M.;
"Assignment of ARI, transcription factor 20 (TCF20), to human chromosome 22q13.3 with somatic cell hybrids and in situ hybridization.";
Cytogenet. Cell Genet. 81:176-177(1998).

I FUNCTION: Transcriptional activator that binds to the regulatory region of MMP3 and thereby controls stromelysin expression. It stimulates the activity of various transcriptional activators as JUN, SPI, PAX6 and ETS1, suggesting a function as a coactivator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOIG=Q9UGUO-2; Sequence=VSP 003984, VSP 003985;
-1- TISSUE SPECIFICITY: Expressed in most tissues, except in ovary and prostate. Isoform 1 is exclusively expressed in brain, heart and testis, and this form predominates in liver and kidney. Isoform 2 predominates in lung.
-1- DOWAIN: The atypical PHD domain functions as a negative modulator of cofactor binding (By similarity).
-1- SIMILARITY: Contains 1 PHD-type zinc finger.
-1- SIMILARITY: Contains 1 PHD-type zinc finger.
-1- CAUTION: Ref. 4 sequence differs from that shown due to a
Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Boderteich A., Hartman K., Hu X., Khan A.S., Lane L., Tilahun Y., Wright H.; "The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                MEDLINE=97323006; PubMed=9179496;
Ohara O., Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Homodimer (Probable). Interacts with RNF4 and JUN (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003677; F:DNA binding; NAS.
GO; GO:0003713; P:transcription coactivator activity; NAS.
GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
InterPro; IPRO01965; Znf_PHD.
SMART; SM00249; PHD; 1.
                                                                                                                                                                                                                                                                                   "Construction and characterization of human brain cDNA libraries
                                                                                                                                                                                                                                                                                          suitable for analysis of cDNA clones encoding relatively large proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
Name=1;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1083-1938 FROM N.A. (ISOFORM 2).
                                                                                                                                                                          SEQUENCE OF 245-1960 FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9UGU0-1; Sequence=Displayed;
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EMBL; AL031346; CAB42440.1; ALT_INIT.
EMBL; AL021878; -; NOT_ANNOTATED_CDS.
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Genew; HGNC:11631; TCF20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
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                                                                                                                               Nature 402:489-495(1999)
                                                                                                                                                                                                                                                                                                                                                  DNA Res. 4:53-59(1997).
                                                                                                                                                                                                                                                             Nomura N.;
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Activator; Alternative splicing; DNA-binding; Nuclear protein;

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Q9EPQB; Q60792;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Transcription factor 20 (Stromelysin 1 PDGF-responsive element-binding
protein) (SPRE-binding protein) (Nuclear factor SPBP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Fibroblast;
MEDLINE=95280915; PubMed=7760812;
Sanz L., Moscat J., Diaz-Meco M.T.;
Wholecular characterization of a novel transcription factor that controls stromelysin expression.";
Mol. Cell. Biol. 15:3164-3170(1995).
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Kirstein M., Sanz L., Moscat J., Diaz-Meco M.T., Saus J.;
Kirstein M., Sanz L., Moscat J., Diaz-Meco M.T., Saus J.;
Cross-talk between different enhancer elements during mitogenic induction of the human stromelysin-1 gene.";
J. Biol. Chem. 271:18231-18236 (1996).
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MEDLINE=20408957; PubMed=10849425; DOI=10.1074/jbc.M003405200;
                                                 (B)
                                                                                                                         (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), CHARACTERIZATION, AND
                                                                                                                                                                        Nuclear localization signal (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.2%; Score 49; DB 1; Length 1960; 47.4%; Pred. No. 1.2e+02;
                         Leucine-zipper.
Nuclear localization signal
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Nuclear localization signal
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Missing (In isoform 2).
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K -> Q (in Ref. 2)
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Poly-Pro.
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regulation; Zinc-finger
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MEDLINE=20568288; PubMed=10995766;
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Interaction between the transcription factor SPBP and the positive Triteraction between the transcription factor SPBP and the positive Triteraction between the transcription factor SPBP and the positive RT offactor RNP4. An interplay between protein binding zinc fingers:";

J. Biol. Chem. 275:26144-26149 (2000).

- I- FUNCTION: Transcriptional activator that binds to the regulatory region of WMP3 and thereby controls stromelysin expression. It stimulates the activity of various transcriptional activators such as JUN, SPI, PAX6 and ETSI, suggesting a function as a coactivator.

- SUBUNIT: Homodimer (Probable). Interacts with RNP4 and JUN. Binds to the regulatory region of MMP3.

- I- SUBCELLUIAR LOCATION: Nuclear. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb.sib.ch). P->S: Loss of interaction with RNF4; when associated with T-1629, R-1736 and V-A->T: Loss of interaction with RNF4; when R EMBL; U20282; AAA6495.1; ALT_SEO.

R GO; GO:000547; F:DNA binding; ISS.

GO; GO:0003713; F:transcription coactivator activity; ISS.

GO; GO:0003713; F:transcription of transcription, DNA-dependent; ISS.

GO; GO:0003713; F:transcription of transcription, DNA-dependent; ISS.

R GO; GO:0006375; PHD; I:DHD; I:DHD; I:DHD; ISS.

R MART; SM00249; PHD; I:DHD; I:DHD; I:DHD; I:DHD; ISS.

Transcription regulation; Zinc-finger.

TowalN ISS ISS Noteration Signal.

TowalN ISS Noteration Signal.

TOWALN INCHART Note: ISS Noteration signal.

TOWALN INCHART NOTE: ISS Note ISS No DOMAIN: The atypical PHD domain functions as a negative modulator of cofactor binding. testes.
DEVELOPMENTAL STAGE: Isoform 2 is exclusively expressed at 7-11
days of development. Isoform 1 is found only at low levels in 15-POLY-Ala.
POLY-Ala.
POLY-Ala.
POLY-GIN.
POLY-GIN.
POLY-GIN.
POLY-PRO.
POLY-GIU.
POLY-GIU.
POLY-GIU.
POLY-GIU. IsoId=Q9EPQ8-2; Sequence=VSP 001986; TISSUE SPECIFICITY: Expressed In brain, lung, liver, kidney and 1737. CG->RV: Loss of interaction with RNF4; SIMILARITY: Contains 1 A.T hook DNA-binding repeat. SIMILARITY: Contains 1 PHD-type zinc finger. CAUTION: Ref.2 sequence differs from that shown due to frameshifts. Nuclear localization signal Nuclear localization signal Event-Alternative splicing; Named isoforms-2, PHD-type (atypical) /FTId=VSP_003986. A->T: Loss of int IsoId=09EPQ8-1; Sequence=Displayed; EMBL; AY007594; AAG28929.1; 1219 1295 1295 1628 1628 1962 1962 195 1629 1702 1737 1684 1797 1983 days embryos.

When associated with T-1629 and S-1702.	2 GSWYSNRKMSHKIRPFPQ 20 	OGGLLS PRELIMINARY, PRT; 313 AA. GGGLLS; GGGLGS; GGGLGS; GGGGLGS; GGGGLGS; GGGGGGGGGG
MUTAGEN MUTAGEN MUTAGEN MUTAGEN SEQUENCE Cuery Match Best Local 8	2 1737	44 66GLLS 66GLLS 66GLLS 66GLLS 66GLLS 66GLLS 67 67 67 67 67 67 67 67 67 67 67 67 67
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Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococales;
Methanocaldococcaceae; Methanocaldococcus.
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SEQUENCE 128 AA, 15567 MW, 462D677CE5B159D3 CRC64;
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| Similarity 35.7%; Pred. No. 12;
10; Conservative 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                Name=rnp4; OrderedLocusNames=MJ0962;
                                                                                                                                                                                  PRT;
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324 GTSYSLKRVEMKIRP 338
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                          GSWYSMRKMSMKIRP 16
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HAMAP; MF 00757; -; 1.
InterPro; IPR007175; Rpr2.
Pfam; PF04032; Rpr2; 1.
                                                                                                                                                                                  STANDARD;
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Alausner R.D., Collins F.S., Wagner i., Shenmen C.M., Schuler G.D.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A phytins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Broaks S.A., McKernan R.J., Marke J.A., Gunzarne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachy J., Halton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
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Skonopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.
                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                     Length 313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC075230; AAH75230.1; -
                SMART; SM00186; FBG; 1.
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
Hypothetical protein.
SEQUENCE 313 Aa; 36214 MW; 4B82C05FE7E14451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 343 AA; 39286 MW; DAC9C39F76F13C84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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41.4%; Score 48; DB 2;
Best Local Similarity 53.3%; Pred. No. 28;
Matches 8; Conservative 5; Mismatches 5
                                                                                                                                   41.4%; Score 48; DB 2;
50.0%; Pred. No. 25;
vative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           343 AA
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22341132; Pubmed=12454917;
Pfam; PF00147; Fibrinogen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2004 (TrEMBLrel. 28, 01-OCT-2004 (TrEMBLrel. 28, 01-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                       | |||::::||:|
291 GWWYSLKSVTMKLR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dev. Dyn. 225:384-391 (2002)
                                                                                                                                                                                                                             2 GSWYSMRKMSMKIR 15
                                                                                                                                                          Local Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rissue=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FISSUE=Brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 initiative.
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  DEDJE9;
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                                                                                                                                                                                Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Science 273:1058-1073 (1996).
-!- FUNCTION: Part of ribonuclease P, a protein complex that generates
mature tRNA molecules by cleaving their 5'ends (By similarity).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
extra-nucleotide from tRNA precursor.
-!- SUBUNIT: Consists of a catalytic RNA component and at least 4
protein subunits (Potential).
-!- SIMILARITY: Belongs to the eukaryotic/archaeal RNase P protein
component 4 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAINEJAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed=8680807;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlawage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,

Overboek R., Kirknes B.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Ulterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
15-JUL_1998 (Rel. 36, Created)
115-JUL_1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ribonuclease P protein component 4 (EC 3.1.26.5) (RNase P component
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AgCP9446.

Name-agCG55756; ORFNames-ENSANGG00000013971;
Anopheles gambiae Brr. PEST.

EURATYOCA: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TAXID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anopheles gambise str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.5%; Score 47; DB 2; Length 308; 43.8%; Pred. No. 36; ive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AAABOLO08986; EAAO0222.1; -.
InterPro: IPR002181; Fibrinogen_C.
Pfan; PP00147; Fibrinogen_C; 1.
SEQUENCE 308 AA; 35657 MW; 1FB23687EBFB85F8 CRC64;
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EMBL, AAABOL000889, EAAO1903.1; -.

Interpro; IPR002181; Fibrinogen C.

Pfam; PP00417; Fibrinogen C; 1.

SEQUENCE 310 AA; 35997 MW; 535335070B722B23 CRC64;
                                                                                                                     01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Name=agCG43338; ORFNames=ENSANGG0000011322;
                                                               308 AA
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ne : 196 secs
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                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||:||::
291 RGSYYSLKSTKMMVRP 306
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293 RGSYYSLKSTKMMVRP 308
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Best Local Similarity 43.0.
The Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 43.8
Matches 7; Conservative
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                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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RESULT 49
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                                                                                                                                                                                                                                                                                                                                                                                                                  Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                          Archaea; Buryarchaeota; Thermococci; Thermococcatea; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cararrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
Gu M.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
Yu J., Han L.H.,
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF218015; AAG17257.1; -.
HSSP, P02671; HFZD.
HSSP, P02671; HFZD.
HSSP, P02671; HFZD.
FFBM; PF00147; Fibrinogen_C; 1.
SMART; SM0186; FBG; 1.
PROSITE; PS00114; FIBRIN_AG_C_DOMAIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome; Hypothetical protein.
SEQUENCE 125 AA; 13657 MW; C6613D9E8D711154 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PH1324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.5%; Score 47; DB 2; 42.1%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.5%; Score 47; DB 2;
56.2%; Pred. No. 28;
ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 AA
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                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98344137; PubMed=9679194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SWYSMRKMSMKIRPFFPQQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Reg. 5:55-76 (1998).
EMBL, APO00006, BAA30430.1, -.
PIR, F71003, F71003.
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226 KGSGYSLKATTMMIRP 241
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les 9; Conservative
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                                                                                                                                                                                 Pyrococcus horikoshii
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                                                                                                                                                                                                                                                                   NCBI_TaxID=53953;
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RESULT 48 **О9НВРЗ**

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Aag65016 Human fib Ad085132 Human-der Aab39176 Human sec Aab39177 Human sec	Respit Human Himan	Human fi Human Pr Human Pr Pancreas	Aar84551 Partial h Aay94009 Amino aci	Abg62851 Ligand/re Adm73982 Ligand/re	Adg62912 ligand/re Adm74055 ligand/re Aab40614 Sequence	Aaw57671 Collagen-	Aaw49716 Protein p	Aaw49721 Protein p Aar80333 Protein p	Aaw57672 Collagen- Aaw49722 Protein p	Aar65759 Rat hepat	Aag65022 Human fib Ad085138 Human-der		Aamieis/ Peptide # Abb35142 Peptide #	Abg50006 Human liv	Aare5760 Human hep	Aar94317 Hepatocyt Aar94316 Hepatocyt	Adl13280 Human ste Aab43637 Human can	Add45362 Rat Prote Add69273 Human fib	Add69274 Human fib								peptide-09.	binding: proliferation;	coagulation; disorder;	ophilia B; ion: cell rrangolantarion:	losis.								
20 4 AAG65016 20 8 AD085132 194 3 AAB39177	0 00 0	1210	m 10	ഗമ	n ω -	101	0	n n	0 0	~	4 ∞	~ 7	4 4	4 V	0 00	7 7	9 6	ر ر	7	OTNOMIND1.14			pentide: 21 AA.			t entry)	C-terminus peptide,	dnus; cell adhesion; cell	betes mellitus; clotting;	tor VIII deficiency; haem	therapeutic structure; research tool; diagnosis.					99WO-US011517.	98US-00084371.		INC.
26 60 51.7 27 60 51.7 28 60 51.7 29 60 51.7	60 51.	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 51. 60 51.	58 50.	ນຜູ້ແ	588	58 50.	588 50.	58 50.	58 50.	57 49. 57 49.	57 49.	56 48.	56 48.	56 48.	56 48. 56 48.	56 48.	56 48. 54 46.	54 46.			RESULT 1	AAYS2600 ID AAYS2600 standard: peptide:	AAY		DT 07-MAR-2000 (first	DE Synthetic fibrinogen					XX OS Synthetic.		PN WO9961041-A1. XX	PD 02-DEC-1999.	26-MAY-1999;	XX PR 27-MAY-1998; 98U	(HADA-)	PA (VITE-) VI TECHNOLOGIES
	-											-												Synthetic	ın-der	Human pro	n fib	n pro	n fib	in fib	n pro	in pro	n pro	n pro n fib	Human fib	ded u	in pep in ang		Human-der
5.1.6 Compugen Ltd.		, Search time 151 Seconds (without alignments) 49.890 Million cell updates/sec						: 2002273											d by chance to have a the result being printed	stribution.			Description	Aay52600 Synt Aaq65028 Hapt	Ado85130 Hume	Aam78493 Hume	Aar82243 Human	Aam/8492 Hume Aae36413 Hume	Adp65229 Hume	Adp65300 Hume	Aam78491 Hume	Ade76868 Human Aam79475 Human	Aam79476 Hume	Aam79477 Human Add69271 Human	Add69272 Hume		o m	0114	Ado85142 Hume
GenCore version 5.1.((c) 1993 - 2005 Compu	using sw model	2005, 11:04:00 ; Seard (withou 49.890	JA-1	SMKIRPFFPQQ 21	Gabext 0.5			ing chosen parameters	00000		ch 0*	st 65 summaries	3Sep04:*	19808:*	20008:*	20018:* 20028:*	2003as:* 2003bs:*		r of results predicted by squal to the score of the	f the	SUMMARIES		DB ID		œ	4 u	· 70 ·	4 6	7	~ 4	4	∞ 4	4	4 1		0 4	4 4	4 4	80
Copyright	protein search,	January 18,	US-09-487-790A-1	e: 116 1 KGSWYSMRKMSMKIRPFFPQQ				of hits satisfying	Beg length: 0 Beg length: 200000000		ing: Minimum Match Maximum Match	Listing fir	A Geneseq 2	١			6: geneseqp2003as:* 7: geneseqp2003bs:*	.: ::		derived b	s	Query	re Match Length	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	97.4	97.4	97.4	94.0	64.7	44	62.1 51.7	51.7
	OM protein -	Run on:	Title:	Perfect score Sequence:	Scoring table	7000		Total number	Minimum DB 80 Maximum DB 80	•	Post-processing		Database :						Pred.)	w		Result	No. Score						. 00	۰.	10	w 4.	2	9 6		. 0	22		

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                                                                                                                                                                                                                                                                                                                                   Corresponds to a fibrinogen beta chain C-terminal sequence. The invention corresponds to a fibrinogen beta chain C-terminal sequence. The invention relates to novel fibrinogen C-terminal peptides, peptide-09 (AAV52600), peptide-70 (AAV52693) and peptide-71 (AAV52694). These claimed peptides can be used to promote healing, and peptide-71 being the next most potent. Peptides of also found to have cell proliferative effects. The peptides can be used to promote healing of a wound in a patient. They can also be used for diseases characterised by the absence of a cellular product, e.g., diseases characterised by the absence of a cellular product, e.g., diseases characterised by the absence of a cellular product, e.g., diseases characterised by the absence of a cellular product, e.g., diseases characterised by the absence of a cellular product, e.g., diseases characterised by the absence of a cellular product, e.g., and hemophilia B (factor IX deficiency). They can also be used for the growth and transport of cells in cell culturing systems, the separation of cells into tissues or cell cultures. They can be used for producing therapeutic structures, e.g., gels, prosthetic devices or collagen sheets. The peptides can also be used as tools for performing analysis of other physiological systems, and for further research and development, for example, to identify and isolate cell receptors. The peptides can also be used in diagnosis, e.g., of blood coagulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, cell attachment peptide; haptotactic; fibrinogen; wound healing
angiopoietin; tenascin; microfibril-associated glycoprotein-4; MFAP4;
cell separation; cell receptor.
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                                                             New peptides corresponding to fibrinogen carboxy terminus, used for promoting wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 21;
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Pred. No. 9.9e-12;
; Mismatches 0;
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                                                                                                   Claim 1; Page 6; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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           Marx
                                   WPI; 2000-062582/05.
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nes 21; Conserv
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             Gorodetsky R,
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                                                                                                                                                                             homologous to sequences found within the C-termini of fibrinogen, and which are characterised by their ability to induce cell attachment to a surface to which the peptide is bound. These are useful in the treatment of wounds and diseases, to separate different types of cells in culture, to analyse cell receptor mechanisms and to design peptide-derivatised drugs. The present sequence is a known haptotactic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haptotactic; liposomal composition; carboxy termini; fibrinogen chain; liposome; lipid bilayer; aqueous compartment; delivery; human.
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                                                                                                                                          present invention provides haptotactic peptides with sequences
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                                                                     Disclosure; Page 14; 43pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 AA;
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osteogenesis
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(DIAD-) DIADEXUS INC
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Best Local Similarity
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               Sequence 453 AA;
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                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; poptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
that of a human-derived haptotactic peptide which may be used during the creation of the compositions of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asundi V, Zhou P, Xu C, Cao Y;
J, Zhang J, Ren F, Chen R, Wang ZW;
Goodrich R;
                                                                                     Gaps
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                                                             Length 21;
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                                                          ; Score 116; DB 8;
; Pred. No. 9.9e-12;
0; Mismatches 0;
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                                                                                                                                                                                                AAM78493 standard; protein; 453 AA.
                                                                                                             1 KGSWYSMRKMSMKIRPFFPQQ 21
                                                                                                                          1 KGSWYSMRKMSMKIRPFFPQQ 21
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27-APR-2000; 2000US-00560875.
20-JUL-2000; 2000US-00598075.
19-JUL-2000; 2000US-0062325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0065351.
20-OCT-2000; 2000US-0069325.
30-NOV-2000; 2000US-0069325.
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Ma Y, Zhao QA, Wang D, Wang
Xue AJ, Yang Y, Wejhrman T,
                                                           100.0%;
                                                                                                                                                                                                                                                                            Human protein SEQ ID NO 1155.
                                                                                                                                                                                                                                                                                                                                                                                                                                        05-FEB-2001; 2001WO-US004098
                                                    Query Match
Best Local Similarity 100.0
Marches 21; Conservative
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                                    Sequence 21 AA;
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                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-1421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, invention are useful for identifying, diagnosing, monitoring, staging, they are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the inng. Invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This is the amino acid sequence of a lung specific nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene therapy, vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer; non-cancerous diseases of the lung; transgenic animal.
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Length 453;
                                                                   Indels
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Query Match 100.0%; Score 116; DB 4; Best Local Similarity 100.0%; Pred. No. 2.6e-10; Matches 21; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 320-322; 389pp; English.
                                                                                                                                                                                                                                                                                                                                                             ABU60918 standard; protein; 489 AA
                                                                                                                                                                                               433 KGSWYSMRKMSMKIRPFFPQQ 453
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                                                                                                                                   1 KGSWYSMRKMSMKIRPFPQQ
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Xu C, Cao Y; , Chen R, Wang ZW;

AAR82243;

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The invention relates to polynuclectides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunoomodulatory activity and activity, tissue growth factor activity, immunoomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leuksemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombospondin 2; THBS2; angiotensin converting enzyme; polymorphism; ACB-1; beta-fibitinogen; FGB; peripheral vascular disease; ischaemia; vascular disease; myocardial infarction; pulmonary embolism; stroke; atherosclerosis; coronary artery disease; venous thromboembolism; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 491;
                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT, Asundi V, Zhou P, Xu
Wang D, Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 116; DB 4;
100.0%; Pred. No. 2.8e-10;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 3389-3390; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                    Wang D, Wang
Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis and gene therapy
                                                                                                                                                                                                           19-JUL-2000; 2000US-00620325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00653561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
                                                                                                        05-FEB-2001; 2001WO-US004098
                                                                                                                                                                   27-APR-2000; 2000US-00560875
20-JUN-2000; 2000US-00598075
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Les 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-476283/51.
N-PSDB; AAK51625.
                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEO INC.
                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C,
Ma Y, Zhao QA, V
Xue AJ, Yang Y,
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                        WO200157190-A2
                                                                                                                                                  03-FEB-2000;
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                                                                 09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human fibrinogen B-beta chain may be produced recombinantly, preferably by sheep beta-lactoglobulin signal peptide fusion protein gene expression in non-human transgenic animal milk, preferably of a sheep, pig, goat or cattle. Co-expression with the fibrinogen A-alpha chain (see AAR82244) and the gamma chain (see AAR82245) results in the production of active fibrinogen, which is useful in human and veterinary medicine, e.g. in the formulation of surgical adhesives, which also consist of Factor-XIII, and as a coating surface for polymeric articles, such as synthetic vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Production of fibrinogen in transgenic mammals - by introducing DNA segments into the germ line of a non-human mammal and collecting milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                Human fibrinogen B-beta chain; transgenic animal milk; treatment; sheep beta-lactoglobulin signal peptide fusion protein; surgical adhesive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; (Page 55-57; 99pp; English.
                                                                                                                          Human fibrinogen B-beta chain protein
AAR82243 standard; protein; 491 AA.
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                                                                                                                                                                                                                                                                                                                                                                                 95WO-US002648.
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                                                                                                                                                                                                                                                                                                                                                                                                                          94US-00206176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZYMO ) ZYMOGENETICS INC. (PHAR-) PHARM PROTEINS LTD.
                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-320582/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from female progeny
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Best Local Simil
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                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1995;
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AAM78492;

AAM78492 RESULT

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The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a Spatient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using the mRNA that cereal signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention of the genes correlates with that of the gene signature. The invention of the genes for targeting in the treatment of theumatoid arthritis; identification of genes for targeting in the treatment of theumatoid arthritis; an ammmal of the cother than a mouse; diagnosis of theumatoid arthritis; diagnosis or arralyses of autoimmune disease or rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; and reducing the symptoms associated with collagentinduced arthritis and reducing the symptoms associated with collagentinduced arthritis. The compositions of the invention have the following activities: immunosuppressive, dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for methods and compositions of the present invention are useful for methods and treating autoimmune disease or arthritides, such as the manner of autoimmune disease caused by an infectious agent. This sequence represents a protein sequence relating to the genes used in the analysis and treatment of autoimmune disease or arthritides. Note: This sequence is not shown and the specification. It has been supplied in an electronic format from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disease; arthritide; gene expression analysis; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antigout; antiinflammatcry; dermatological; immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis; immune; human.
                                                                                                                                                                                                                                                                                                Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 116; DB 7;
100.0%; Pred. No. 2.8e-10;
ive 0; Mismatches 0;
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                                                                                                          (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP65300 standard; protein; 491 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page; 56pp; English.
                                                        31-OCT-2001; 2001US-0336220P.
  31-OCT-2002; 2002WO-US035433
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Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                               Thorton St.
                                                                                                                                                                                                                  WPI; 2003-712740/67.
                                                                                                                                                                                                                                                 GENBANK; NP_005132
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                                                                                                                                                               Hirsch R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying polymorphisms in thrombospondin 2, angiotensin converting enzyme and/or beta-fibrinogen genes in nucleic acid sample of subject, contacting the nucleic acid with a complementary probe or primer.
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                         /note= "This residue is changed to Lys due to single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 116; DB 6;
100.0%; Pred. No. 2.8e-10;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Fig 6; 194pp; English
                                                                                                                                                                                                               04-SEP-2002; 2002WO-US028113.
                                                                                                                                                                                                                                                               05-SEP-2001; 2001US-0317178P.
16-OCT-2001; 2001US-0329958P.
14-DEC-2001; 2001US-00017724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    appear to be the case
                                                                                                                                                                                                                                                                                                                                                                         (VITI-) VITIVITY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-300816/29.
Misc-difference 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 21: Сопянт
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                                                                                                       WO2003020118-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo Bapiens
                                                                                                                                                          13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mccarthy J;
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Gaps

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04-SEP-2003

ADP65229;

RESULT 9 ADP65229

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8

Query Match

Length 491; Indela

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent of for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. We ctors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins care useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. ANU29510-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; accine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding a range of human polypeptides, useful in genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 430; 765pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM78491 standard; protein; 539 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein SEQ ID NO 1153.
                                                                                                                                                                                                                                          16-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                           18-APR-2000; 2000US-00552929 26-JAN-2001; 2001US-00770160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-611725/70.
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                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 502 AA;
                                                                                                                              WO200179449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157190-A2
                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for diagnosing and analysing a utcoimmune disease or arthritides. The method comprises obtaining a CC patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that correspond in the patient, where gene expression of at least 60% of cor arthritides in the patient, where gene expression of alleast 60% of the genes correlates with that of the gene signature. The invention of the genes for targeting in the treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis; diagnosis or array or gene chip, specific for rheumatoid arthritis; diagnosis or array or gene chip, specific for rheumatoid arthritis; accening the cfficacy of a candidate drug in vitro for the treatment of collagentinduced arthritis, and reducing the symptoms associated with collagentinduced arthritis. The compositions of the invention have the following activities: immunsuppressive, antirheumatic, antiantides, such as call and treating autoimmune disease or arthritides, such as themselved arthritis, and treating autoimmune disease or arthritides, such as chemmatoid arthritis, and and disease caused by an infectious agent. This sequence represents a confusion of the genes used in the analysis and treatment of mine disease caused by an infectious agent. This sequence is not shown and composition. It has been supplied in an electronic format from and the propersory and the propersory of an arthritides such as the propersory of an arthritides. The composition of the genes used in the analysis and treatment of an the propersory of an arthritides. The sequence relating to the genes used in the analysis and treatment of an anthritides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Pred. No. 2.8e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU31380 standard; protein; 502
                                                                                                                                                       31-OCT-2002; 2002WO-US035433
                                                                                                                                                                                                           31-OCT-2001; 2001US-0336220P
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                                                                                                                                                                                                                                                                                                                 Hirsch R, Thorton SL;
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-712740/67.
                                                                                                                                                                                                                                                                                                                                                                                              GENBANK; NP_005132.
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                                                 WO2003072827-A1
Homo sapiens
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Local Sim
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                                                                                                     04-SEP-2003
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Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 33; 41pp; English.
                          28-JUL-2000; 2000US-0222113P.
                                                                                                                                                             WPI; 2004-031227/03
                                                                     (KASE/) KASER M R.
                                                                                                                                                                                   N-PSDB; ADE76867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver disorder.
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27-APR-2000; 2
20-JUN-2000; 2
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                                                                                                                                                                                                                                                                              disorders.
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                                                                                                                  Kaser MR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
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                                                                                                                                                                                                                                                                                                                                       Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein expressed in a liver disorder #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 3388-3389; 6221pp; English.
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                                                                                   03-FEB-2000; 2000US-00496914.
27-AFR-2000; 2000US-00560875.
20-UN-2000; 2000US-0059075.
19-JUL-2000; 2000US-00630325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0065351.
20-CT-2000; 2000US-00693355.
30-NOV-2000; 2000US-00728422.
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                                             05-FEB-2001; 2001WO-US004098
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                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAK51624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 539 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003108871-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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ADE76868
PRAKE 
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The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for for treating liver disorder such as hyperlaidemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a CDNA. A protein encoded by the CDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid is a protein encoded by a cDNA differentially expressed in a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 KGSWYSMKKMSMKIRPFFPQQ 488
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2000US-00560875.
2000US-00598075.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.4.
Best Local Similarity 95.2<sup>*</sup>
Matches 20; Conservative
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15-SEP-2000; 2000US-00663561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
                                                (HYSE-) HYSEQ INC
                                                                                                                                  N-PSDB; AAK52609
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 495 AA;
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20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM79477;
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                                                                                                                                                                                Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                              Y;
Wang ZW;
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                                                                                               Xu C, Cao,
Chen R,
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                                                                                           Tang YT, Liu C, Drmanac RT, Agundi V, Zhou P, Xv
Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F,
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                 Claim 20; Page 257-258; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 KGSWYSMKKMSMKIRPFFPQQ 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM79476 standard; protein; 495 AA.
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19-JUL-2000; 2000US-00620325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00653561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
                                                                                                                                                                                          in diagnosis and gene therapy
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27-APR-2000; 2000US-00560B75.
20-UUN-2000; 2000US-0059075.
19-UUL-2000; 2000US-00520325.
01-SEP-2000; 2000US-00654936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein SEQ ID NO 3122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.4
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                          WPI; 2001-476283/51.
                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                       N-PSDB; AAK52608
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 495 AA;
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The invention relates to polynucleotides (AAK51456-AAK51435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to ercoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to production of location or call differentiation or which may induce production of other cytokines in other cell populations. The polymetides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides with cytokine-like activities, useful
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    Y;
Wang ZW;
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Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.4%; Score 113; DB 4; Length 495; Best Local Similarity 95.2%; Pred. No. 8.9e-10; Matches 20; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 258; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM79477 standard; protein; 495 AA
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                                                                                                                                                                                                                                                                                                                        in diagnosis and gene therapy.
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2000US-00598075.
2000US-00620325.
2000US-00654936.
2000US-006693325.
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94.0%;
95.2%;
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                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                    Query Match
Best Local Similarity 95.2
Matches 20; Conservative
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                                                                                                                                                                                 Sequence 491 AA;
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                                                                                                                                                                                                                            production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                        The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion protein; fibrinogen-like; coiled-like domain; ang-2; Ang-3; angiopoietin-related factor; ARF; angiopoietin; Ang-1; Ang-2; Ang-3; Ang-4; Ang-2X; vulnerary; antiinflammatory; vasotropic; necrosis; ischaemia; inflammation; wound healing; CCD; FLD; human; fibrinogen beta.
                                                                                                                               Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                              Y;
Wang ZW;
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                                             ', Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                       Score 113; DB 4; Length 495;
Pred. No. 8.9e-10;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human fibrinogen beta protein 1 - SEQ ID 7.
                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                   Claim 20; Page 258; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 KGSWYSMKKMSMKIRPFFPQQ 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD69271 standard; protein; 491 AA
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                                                                                                                                             in diagnosis and gene therapy
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Best Local Similarity 95.2%;
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30-NOV-2000; 2000US-00728422
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                                                                                             WPI; 2001-476283/51.
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                      (HYSE-) HYSEQ INC
                                                                                                         N-PSDB; AAK52610
                                                                                                                                                                                                                                                                                                                                                                  Sequence 495 AA;
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                                             Tang YT,
Ma Y, Zh
                                                                     Xue AJ,
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The invention relates to a novel fusion protein comprising a fibrinogen-
like domain (FLD) or colled-coil domain (CCD). The domain may be
identical or homologous to that of an angiopoietin-related factor (ARF),
examples of which include Ang (angiopoietin)-1, Ang-2, Ang-3, Ang-4 and
Ang-2x. The molecules of the invention demonstrate vulnerary,
antiinflammatory and vasotropic activities whilst the fusion protein may
be useful for preparing a composition for treating necrosis, ischaemia or
inflammation, as well as for promoting wound healing. The current
sequence is that of the human fibrinogen beta protein of the invention.
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like domain (FLD) or coiled-coil domain (CCD). The domain may be
identical or homologous to that of an anglopolatein-related factor (ARF),
examples of which include Ang (anglopolatin)-1, Ang-3, Ang-4 and
Ang-2x. The molecules of the invention demonstrate vulnerary,
antiinflammatory and vasotropic activities whilst the fusion protein may
be useful for preparing a composition for treating necrosis, ischaemia or
inflammation, as well as for promocing wound healing. The current
sequence is that of the human fibrinogen beta protein of the invention.
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Ang-4; Ang-2X; vulnerary; antiinflammatory; vasotropic; necrosis;
ischaemia; inflammation; wound healing; CCD; FLD; human; fibrinogen beta.
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useful for preparing a composition for treating necrosis, ischemia or inflammation, or for promoting wound healing.
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Pred. No. 4e-09;
0; Mismatches 1; Indels
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                                                                                                                                                Disclosure, SEQ ID NO 7; 340pp; English.
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Query Match Matches

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ADI82107

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The present invention relates to oligonucleotides (see AAL26793-AAL34659)
encoding polymorphic variants of proteins related to amylases, amyloid
proteins, anglopoleith, apoptosis related proteins, cadherin, cyclin,
polymerase, oncogenes, histones, kinases, colony stimulating factors,
complement related proteins, cytochromes, kinesins, cytokines,
interleukins, G-protein coupled receptors and thioesterases.
The present sequence is a peptide encoded by them may be used in the
prevention, diagnosis and treatment of diseases associated with
prevention, diagnosis and treatment of diseases associated with
prevented, diagnosed and/or treated include multifactorial diseases
with a genetic component, such as autoimmune diseases (e.g. rheumatoid
arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus
and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
brain, breast, colon and kidney, leukaemia), diseases of the nervous
                                                                                                                                                                                                                                   neuroprofective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoletin; apoptosis related protein; cadherin; cyclin; polymerses; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukh; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                                                                                                                                                                                                                  Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                         Human peptide #315 encoded by a SNP oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 75; DB 4; Le
Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.7%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 3737; 4143pp; English.
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                                        AAM97040 standard; peptide; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-2000; 2000WO-US035498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-DEC-1999; 99US-0173419P.
27-DEC-2000; 2000US-00173419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GSWYSMRKMSMKIR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSWYSMRKMSMKIR 14
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                   nervous system disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-465210/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200147944-A2
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimkets RA,
                                                                                                                               24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2001.
                                                                                    AAM97040;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM97039
ID AAMS
                      AAM97040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 kidney toxicity; T-kinninogen; inter-alpha-inhibitor H4P heavy chain; alpha-1-macroglobulin; apolipoprotein E; clusterin; complement C3; complement C4; fibrinogen-alpha-chain; fibrinogen-beta-chain; plasma retinol binding protein; renal tubular necrosis; drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises a method for screening or diagnosing kidney toxicity. The method involves the use of the following proteins: Thiningoen, inter-alpha-inhibitor H4P heavy chain, alpha-1-macroglobulin, appolipoprotein E, clusterin, complement C3, complement C4, fibrinogenalpha-chain, fibrinogen-beta-chain, and plasma retinol binding protein. The method of the invention is useful in screening or diagnosing kidney coxicity (e.g. renal tubular necrosis). The method is also useful for monitoring the effectiveness of treatment for kidney toxicity and for screening and developing drugs. The present amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening or diagnosing kidney toxicity, useful in monitoring effectiveness of treatment for kidney toxicity or for screening and developing of drugs, by detecting and quantifying T-kininogen and inter-
                                                                                    Gaps
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0
                                        94.0%; Score 109; DB 7; Length 491; 95.2%; Pred. No. 4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 479;
                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Pred. No. 1.2e-08;
1; Mismatches 1;
                                                              Pred. No. 4e-09;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 10; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                              ADI82107 standard; protein; 479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGSWYSMRRMSMKIRPVFPQQ 479
                                                                                                                                                       1 KGSWYSMRKMSMKIRPFFPQQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KGSWYSMRKMSMKIRPFFPQQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha-inhibitor H4P heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                         Fibrinogen-beta-chain protein.
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                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                  20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-099412/10.
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Best Local Similarity
Matches 19; Conserv
                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 479 AA;
Sequence 491 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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Gaps

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ò 셤 01-OCT-2001 (first entry)

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prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms
                                                                                                                             Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; miterfleukin; G-protein coupled receptor; thioesterase; intlammation; nervous system disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, interferons, interferons, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioseterases. The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 75; DB 4; Length 14;
Pred. No. 3.3e-05;
0; Mismatches 0; Indels
                                                                                            Human peptide #314 encoded by a SNP oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 3736; 4143pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.7%; Sco...
100.0%; Pred
0; N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-1999; 99US-0173419P.
27-DEC-2000; 2000US-00173419.
                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-2000; 2000WO-US035498.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-465210/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                              WO200147944-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA,
                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2001
                  AAM97039;
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Matches
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The present invention relates to human nucleic acids containing single nucleotide polymorphisms (SNPs). These can be used in forensic and paternity tests, and to aid in the treatment of diseases associated with aberrant protein expression, including cancer, amyloidosis, diabetes, Alzheimer's disease, Down's syndrome, oedema, lupus (SLB), vasculitis, alpmerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis, meningitis, muscular disorders, dementia, neurological diseases, tuberous sclerosis, male infertility, hypercalcaemia, blood pressure disorders, autoimmunity. The present sequence is a peptiide encoded by a polymorphism-containing oligonucleotide fragment of the invention
                                                                                                                                                                                                                                                                                                                                                Isolated human polynucleotides containing single nucleotide polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, single nucleotide polymorphism, SNP, paternity test, forensic test; aberrant protein expression.
                                                      Human, single nucleotide polymorphism, SNP, paternity test,
forensic test, aberrant protein expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 75; DB 4; Length 14;
Pred. No. 3.3e-05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human angiopoietin fragment SEQ ID NO: 654.
                           Human angiopoietin fragment SEQ ID NO: 653
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 293; 475pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.7%; Sc.
100.0%; Pre/
0; h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JAN-2001; 2001WO-US000322.
                                                                                                                                                                                                                   07-JAN-2000; 2000US-0174962P
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                                                                                                                                                                                                                                                                             Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                              infection and diabetes.
                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                        WPI; 2001-451871/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                      N-PSDB; AAH89222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14 AA;
                                                                                                                              WO200151670-A2.
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                                                                                                    Ното варіепв.
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                                                                                                                                                           19-JUL-2001.
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Gaps ö

AAM00113;

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The present invention provides haptotactic peptides with sequences homologous to sequences found within the C-termini of fibrinogen, and which are characterised by their ability to induce cell attachment to a surface to which the peptide is bound. These are useful in the treatment of wounds and diseases, to separate different types of cells in culture, to analyse cell receptor mechanisms and to design peptide-derivatised drugs. The present sequence is a consensus sequence of haptotactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haptotactic peptide liposomal composition, useful for enhancing liposome uptake into cells, comprising peptide capable of eliciting cell attachment responses and sequence similarity to haptotatic peptides and liposome having lipid bilayers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haptotactic; liposomal composition; carboxy termini; fibrinogen chain;
liposome; lipid bilayer; aqueous compartment; delivery; human.
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "OTHER= Non-charged amino acid or optionally
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                                                                                                                                                                                                                          Length 16;
                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human-derived consensus haptotactic peptide SeqID13.
                                                                                                                                                                                                                          Score 60; DB 4;
Pred. No. 0.011;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO85142 standard; peptide; 16 AA.
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                                                                                                                                                                                                                          51.7%;
75.0%;
                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                                          || || || || || || || || KGXXYSMRKIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                    1 KGSWYSMRKMSMKIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HAPT-) HAPTO BIOTECH INC.
                                                                                                                                                                                                                                             Local Similarity 75.0
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "absent"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                        Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD085142;
                                                                                                                                                 peptides
                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                  nucleotide polymorphisms (SNPs). These can be used in forensic and paternity tests, and to aid in the treatment of diseases associated with aberrant protein expression, including cancer, amyloidosis, diabetes, Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis, alzheimer's disease, Down's syndrome, trormbocytopenia, arthritis, meningitis, mascular disorders, dementia, neurological diseases, tuberous scleropsis, male infertility, hypercalcaemia, blood pressure disorders, autoimmunity. The present steepunce is a peptide encoded by a polymorphism-containing oligonucleotide fragment of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cell attachment peptide; haptotactic; fibrinogen; wound healing; angiopoietin; tenascin; microfibril-associated glycoprotein-4; MFAP4; cell separation; cell receptor.
                                                                                                                                                                                                                                                                                                  present invention relates to human nucleic acids containing single
                                                                                                                                                                                    Isolated human polynucleotides containing single nucleotide polymorphisms, useful for the treatment and diagnosis of e.g. cancer, infection and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.1%; Score 72; DB 4; Length 14; 92.9%; Pred. No. 0.0001; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RES SERVICES & DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haptotactic peptide consensus sequence #1
                                                                                                                                                                                                                                                               Disclosure; Page 293; 475pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG65026 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 7; 43pp; English.
               07-JAN-2000; 2000US-0174962P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-2001; 2001WO-IL000057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JAN-2000; 2000US-00487790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GSWYSMRKMSMKIR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                          Leach MD
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                                                     (CURA-) CURAGEN CORP.
                                                                                                                             WPI; 2001-451871/48.
N-PSDB; AAH89223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-457595/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
tes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14 AA;
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                                                                                          Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteogenesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG65026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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This invention relates to a novel haptotactic peptide liposomal composition, which comprises at least one type of peptide and one type of liposome, where the peptide elicits cell attachment responses and has an amino acid sequence that is at least 60% homologous to a haptotactic peptide present within the carboxy termini of fibrinogen chains, and the liposome has at least one lipid bilayer enclosing an aqueous compartment. The invention is useful for enhancing liposome uptake into cells or for enhancing intracellular uptake of biologically active composition by low-permeability through the cell membrane using a haptotactic-peptide liposomal composition. The invention may be particularly useful for enhancing the delivery of paramaceutical agent into cells, for enhancing the delivery of paramaceutical agent into cells, for enhancing the delivery of paramaceutical agent into cells, where the liposomes of the composition have a commetic beneficial effect. The present sequence is that of a human-derived haptotactic peptide which may be used during the creation of the compositions of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides haptotactic peptides with sequences homologous to sequences found within the C-termini of fibrinogen, and which are characterised by their ability to induce cell attachment to a surface to which the peptide is bound. These are useful in the treatment of wounds and diseases, to separate different types of cells in culture, to analyse cell receptor mechanisms and to design peptide-derivatised drugs. The present sequence is a homologue of a human fibrinogen C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, cell attachment peptide; haptotactic; fibrinogen; wound healing; angiopoletin; tenascin; microfibril-associated glycoprotein-4; MFAP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel haptotactic peptides useful for enhancing wound healing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.7%; Score 60; DB 8; Length 16; llarity 75.0%; Pred. No. 0.011; Conservative 0; Mismatches 4; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human fibrinogen C-terminus homologue preCgamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HADA-) HADASIT MEDICAL RES SERVICES & DEV
                     Claim 6; SEQ ID NO 13; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG65016 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 6; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell separation; cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2001; 2001WO-IL000057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KGXXYSMRKXXMKIRP 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KGSWYSMRKMSMKIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gorodetsky R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-457595/49.
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200153324-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 26
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This invention relates to a novel haptotactic peptide liposomal composition, which comprises at least one type of peptide and one type of liposome, where the peptide elicits cell attachment responses and has an amino acid sequence that is at least 60% homologous to a haptotactic peptide present within the carboxy termini of fibringen chains, and the liposome has at least one lipid bilayer enclosing an aqueous compartment. The invention is useful for enhancing liposome uptake into cells or for enhancing intracellular uptake of biologically active compounds by low-permeability through the cell membrane using a haptotactic-peptide liposomal composition. The invention may be particularly useful for enhancing the delivery of paramaceutical agent into cells, for enhancing the delivery of paramaceutical agent into cells or for enhancing the delivery of paramaceutical agent into cells or for enhancing commetically effective liposomes into cells, where the liposomes of the composition have a cosmetic beneficial effect. The present sequence is that of a human-derived haptotactic peptide which may be used during the creation of the compositions of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haptotactic peptide liposomal composition, useful for enhancing liposome uptake into cells, comprising peptide capable of eliciting cell attachment responses and sequence similarity to haptotatic peptides and
                                                                                                                                                                                                                                                                                                                                                                                                                      haptotactic, liposomal composition; carboxy termini; fibrinogen chain; liposome; lipid bilayer; aqueous compartment; delivery; human.
                                                                                                           Gaps
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                                                                     Length 20;
                                                                                                         4; Indels
                                                                       DB 4;
                                                                     51.7%; Score 60; DB 4; 64.7%; Pred. No. 0.014;
                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  Human-derived haptotactic peptide SeqID3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           liposome having lipid bilayers.
                                                                                                                                                                                                                                                                          ADO85132 standard; peptide; 20
                                                                                                                                             1 KGSWYSMRKMSMKIRPF 17
                                                                                                                                                                03-NOV-2003; 2003WO-IL000911.
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                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                         11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-449501/42.
                                                                   Query Match
Best Local Similarity
 terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004041298-A1.
                                     Sequence 20 AA;
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                                                                                                           Matches
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Gaps

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Gaps

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4; Indels

51.7%; Score 60; DB 8; Length 20; 64.7%; Pred. No. 0.014;

2; Mismatches

1 KGSWYSMRKMSMKIRPF 17

11; Conservative

Matches

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Local Similarity

Query Match

Sequence 20 AA;

RESULT

| |||||:||:||||| 1 KTRWYSMKKTTMKIIPF 17

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The invention relates to the isolation of genes AAC73865-C73913 encoding the human secreted proteins AAB39093-B39141. This sequence represents a pertide fragment homologous to the protein encoded by the gene isolated in the present invention. The sequence is a search result from a BLASTX homology search. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of:

(a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections
                                                                                                                                                                               Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticonvulsant; antibeterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Forty-nine polynucleotide sequences, and their encoded secreted polypeptides, used in the treatment and diagnosis of cancers, autoimmune
                                                                                                                                        secreted protein BLAST search protein SEQ ID NO: 143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.7%; Score 60; DB 3; Length 194; 64.7%; Pred. No. 0.15; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 407; 413pp; English.
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                     Ą
                 AAB39176 standard; protein; 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides, used in the treal
disorders, and skin disorders.
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                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-594649/56
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                                                                                                                                                                                                                                                                                                                                                 WO200058513-A1.
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17-DEC-1999;
                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                  02-FEB-2001
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                                                         AAB39176;
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AAB39176
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The invention relates to the isolation of genes AAC73865-C73913 encoding the human secreted proteins AAB3903-B39141. This sequence was used as a query sequence for doing BLASTX searches to determine homologous sequences to the protein isolated in the present invention. The genes and sequences to the protein or gene therapy. The genes are isolated from conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the alagnosis, proteins, and other cancers of the adrenal gland, bone, bone ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic
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                                                                                                                                                                      Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antinflammatory; antiulcer; vulnerary; anticonvulsant; antiacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Forty-nine polynucleotide sequences, and their encoded secreted polypeptides, used in the treatment and diagnosis of cancers, autoimmune disorders, and skin disorders.
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0
                                                                                                                                   Human secreted protein BLAST search protein SEQ ID NO: 144.
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64.7%; Pred. No. 0.15;
iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 407-408; 413pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Komatsoulis G;
                  AAB39177 standard; protein; 194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ||||:| :||| ||
156 KTRWYSMKKTTMKIIPF 172
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17-DEC-1999; 99US-0172412P.
                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-2000; 2000WO-US007506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KGSWYSMRKMSMKIRPF
                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-594649/56.
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                                                                                                                                                                                                                                                                                                                                WO200058513-A1
                                                                                             02-FEB-2001
                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                        AAB39177;
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RESULT 30 ADK70498

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11; Conservative

Similarity

Local Best Loca Matches

06-MAY-2004

ADK70498;

Homo sapiens

11-DEC-2003.

Rickert PK,

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The invention relates to a novel predictor set comprising a plurality of polymucleotides and/or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. The molecules of the invention demonstrate cytostatic, antiangiogenic, vasotropic and vulnerary activities and may be useful in the field of pharmacogenomics, in particular for determining drug sensitivity and in treating breast cancer, hypervascular diseases, angiogenesis and scars in wound healing. The current sequence is that of a human protein tyrosine kinase biomarker protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibrinogen gamma' chain; transgenic animal milk; treatment; beta-lactoglobulin signal peptide fusion protein;
                                                                                                                                                                                                                                                                                                                                           New predictor sets with a plurality of polynucleotides and/or polypeptides whose expression pattern predicts cell response to a compound that modulates protein tyrosine kinase activity, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.7%; Score 60; DB 8; Length 437; 64.7%; Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garner I, Dalrymple MA, Prunkard DE, Foster DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.37; ; Mismatches
                                                                                                                                                                                                                     Reeves KA, Amler L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; SEQ ID NO 171; 649pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human fibrinogen gamma' chain protein.
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                                                                                         26-AUG-2003; 2003WO-US026491.
                                                                                                                                                                         (BRIM ) BRISTOL-MYERS SQUIBB
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                                                                                                                                 27-AUG-2002; 2002US-0406385P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 KTRWYSMKKTTMKIIPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC. (PHAR-) PHARM PROTEINS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KGSWYSMRKMSMKIRPF
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                                                                                                                                                                                                                                                                                                                                                                                                              treating breast cancer.
                                                                                                                                                                                                                                                                                 WPI; 2004-239171/22.
N-PSDB; ADL61110.
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                                                                                                                                                                                                               Huang F, Han X,
Shaw P;
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      WO2004020583-A2
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                                              11-MAR-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to CDNA sequences that are differentially expressed in respiratory disorders or their complements or encoded proteins. The CDNAs and proteins are useful for diagnosing, treating or monitoring treatment of a subject with a respiratory disease including lung cancer, chronic obstructive pulmonary diseases, emphysema or asthma. The protein is also useful for screening molecules or compounds to identify at least one ligand which specifically binds the protein. It is also useful for preparing and purifying a polyclonal or monoclonal antibody. This sequence corresponds to a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predictor set; protein tyrosine kinase; cytostatic; antiangiogenic; vaotropic; vulherary; pharmacogenomic; drug sensitivity; breast cancer; hypervascular disease; angiogenesis; wound healing scar; human; biomarker; fibrinogen gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New combination comprising cDNAs and proteins that are differentially expressed in respiratory disorders, useful for disgnosing or treating respiratory diseases e.g. lung cancer, chronic obstructive pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                    cytostatic; respiratory; antiasthmatic; gene therapy; differential gene expression; respiratory disorder; lung cancer; chronic obstructive pulmonary disease; emphysema; asthma.
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Pred. No. 0.37;
2; Mismatches 4; Indels
                                                                                                                            Respiratory disease differentially expressed protein #64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; SEQ ID NO 234; 343pp; English.
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ADK70498 standard; protein; 437
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                                                                                    (first entry)
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nes 11; Conservative
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03-JUN-2004

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                                                                                                                                         The alternatively spliced human fibrinogen gamma' protein is produced by alternative splicing at nucleotides 9511 and 10054 of AAT03854 resulting in translation terminating after nucleotide 10065. Human fibrinogen gamma' chain may be produced recombinantly, preferably by sheep betalactoglobulin signal peptide fusion protein gene expression in non-human transgenic animal milk, preferably of a sheep, pig, goat or cattle. Coexpression with the fibrinogen A-alpha chain (see AAR8244) and the B-beta chain (see AAR82243) results in the production of active fibrinogen, which is useful in human and veterinary medicine, e.g. in the formulation of surgical adhesives, which also consist of Factor-XIII, and as a coating surface for polymeric articles, such as synthetic vascular grafts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human fibrinogen gamma chain may be produced recombinantly, preferably sheep beta-lactoglobulin signal peptide fusion protein gene expression
                                                    Production of fibrinogen in transgenic mammals - by introducing DNA segments into the germ line of a non-human mammal and collecting milk from female progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Production of fibrinogen in transgenic mammals - by introducing DNA segments into the germ line of a non-human mammal and collecting milk from female progeny.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                        Length 453;
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                                                                                                                                                                                                                                                                                                                                                      51.7%; Score 60; DB 2 64.7%; Pred. No. 0.38;
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                  Disclosure; Page 67-69; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human fibrinogen gamma chain protein.
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ses 11; Conservative
            WPI; 1995-320582/41.
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                          N-PSDB; AAT03854.
                                                                                                                                                                                                                                                                                                                          Sequence 453 AA;
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a compound for identifying a compound or small molecule that regulates the
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non-human transgenic animal milk, preferably of a sheep, pig, goat or cattle. Co-expression with the fibrinogen A-alpha chain (see AAR82244) and the B-beta chain (see AAR82243) results in the production of active fibrinogen, which is useful in human and veterinary medicine, e.g. in the formulation of surgical adhesives, which also consist of Factor-XIII, and as a coating surface for polymeric articles, such as synthetic vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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                                                                                                                                                                                                                 51.7%; Score 60; DB 2; Length 453; 64.7%; Pred. No. 0.38;
                                                                                                                                                                                                                                                            4; Indels
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                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Protein P02679, SEQ ID NO 10797.
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KTRWYSMKKTTMKIIPF 415
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                            11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-268312/26
                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                         Sequence 453 AA;
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activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising at least one polypeptide selected from 55 proteins up-
regulated in pancreatic cancer (Table 2 and Table 3, given in the
specification) or from 68 proteins with higher levels in pancreatic
cancer compared to normal tissue (Table 6, given in the specification).

(I) is a polypeptide for use as a marker or as a component of a marker
for diagnosis of pancreatic cancer and/or the susceptibility to
pancreatic cancer. A compound (antibody, an antibody-derivative, an
antibody fragment, a peptide, or an antisense construct) identified by
screening methods using (I) is useful for treatment or prevention of
pancreatic cancer. It is also useful for the preparation of a diagnostic
composition for diagnosing pancreatic cancer or a predisposition for
pancreatic cancer. The current polypeptides were found to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis; pancreatic cancer; antibody; antisense construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a marker (I) for diagnosis of pancreatic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New specific markers comprises at least one polypeptide up-regulated in pancreatic cancer, useful for diagnosing pancreatic cancer.
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                                                                                                                                                                                                                                                                                                    DB 7; Length 453;
0.38;
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CO LTD CHINESE NAT HUMAN GEN.
                                                                                                                                                                                                                                                                                                51.7%; Score 60; DB llarity 64.7%; Pred. No. 0.38 Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 66; 381pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ30579 standard; protein; 453 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                        415
                                                                                                                                                                                                                                                                                                                                                                                  1 KGSWYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-DEC-2003; 2003WO-EP014057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002EP-00028058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-2003; 2003EP-00025237
                                                                                                                                                                                                                                                                                                                                                                                                                    399 KTRWYSMKKTTMKIIPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; diagnosis; r
differential expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HOFF ) HOFFMANN LA (SINO-) SINOGENOMAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-488121/46.
                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                 Sequence 453 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004055519-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-SEP-2004
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                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variant chains of fibrin unable to self polymerise - are able to react with fibrinogen, partic. useful in surgical sealants that do not require
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human fibrinogen; gamma-chain; synthetic 3'-end fragment;
Bluescript II KS+; plasmid; mp19gamma2; expression vector; pREP9;
variant fibrin chains; unable to self polymerise; fibrinogen;
surgical sealants; thrombin activation; pure starting material;
fibrin-derived factors; regulation; angiogenesis; platelet aggregation.
differentially expressed in pancreatic tissue obtained from individuals suffering from pancreatic cancer as compared to healthy pancreatic tissue. They have been identified as ultable as markers of pancreatic cancer for early disgnosis of the disease. This sequence corresponds to
                                                                                                                                                                                    Gaps
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                                                                                                                                                 51.7%; Score 60; DB 8; Length 453; 64.7%; Pred. No. 0.38;
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                                                                                                                                                                                    4; Indels
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Pred. No. 0.38;
                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Partial human fibrinogen gamma-chain.
                                                                                                                                                                                                                                                                                                                                                     AAR84551 standard; protein; 454 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 7; 102pp; English.
                                                                        protein marker of the invention
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KTRWYSMKKTTMKIIPF 415
                                                                                                                                                                                                                        1 KGSWYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SQUI ) SQUIBB & SONS INC E R.
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activation of thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cederholm-Williams SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-392917/50.
                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT05310.
                                                                                                             Sequence 453 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                           399
                                                                                                                                                 Query Match
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Sallberg M, Flock J;
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                                                                                                                                                                                                                                     (TRIP-) TRIPEP AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 AA;
                                                                                                                                                 WO200224887-A2
                                21-AUG-2002
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                                                                                                                                                                      28-MAR-2002
                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM73982;
           ABG62851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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ADM73982
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                                                                                                                                                                                                                                                                                                                                                                                             polymerize but forms non-covalent bond with fibrinogen, useful in surgery for controlling bleeding or adhering tissues to each other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sealant comprises a recombinant variant fibrin chain differing from the naturally occurring gamma-chain by one or more mutations or deletions in a creaminal region following a colled-coll forming region. When incorporated into a fibrin-homologue, the homologue cannot self-polymerize but forms non-covalent bonds or polymerize with fibrinogen. The fibrin sealants are used in surgery to control bleeding or to adhere two tissues to each other. The recombinant fibrin chains are used may be used in the preparation of safe and convenient surgical adhesives and sealants, and as sources of substantially pure starting material for the production of fibrin-derived factors that regulate angiogenesis, or platelet aggregation. Fibrin and fibrin homologues may be used as components of fibrin monomer-based surgical sealants
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the gamma chain of human fibrinogen. The sequence was used to produce a fibrin sealant. The specification describes a fibrin sealant which contains a human fibrin-homologue. The
                                                                                                                                                                              Fibrin sealant; fibrin; surgery; bleeding; adhesion; surgical adhesive; angiogenesis; platelet aggregation; gamma-fibrinogen.
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                                                                                                                                                           Amino acid sequence of the gamma chain of human fibrinogen.
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 Indels
  4
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Pred. No. 0.38;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG62851 standard; peptide; 20 AA.
                                                                                            AAY94009 standard; protein; 454
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5
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                                                                                                                                                                                                                                                                                                  94US-00236979
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ilarity 64.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KGSWYSMRKMSMKIRPF
                                        416 KTRWYSMKKTTMKIIPF
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                                                                                                                                       (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                          Cederhom-Williams SA;
                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-464370/40.
N-PSDB; AAA57835.
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Best Local Similarity
Matches 11; Conser
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                                                                                                                                      20-OCT-2000
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                             03-MAY-1995;
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                                                                                                                                                                                                                                   JS6083902-A.
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11;
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ABG62851
Matches
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The present invention relates to ligand/receptor specificity exchangers comprising at least one specificity domain comprising a ligand for a receptor, and at least one antigenic domain joined to the specificity domain, where the antigenic domain comprises an epitope of a pathogen or toxin. The ligand/receptor specificity exchangers redirect antibodies to receptors present on pathogens. They are useful for preventing and treating human diseases such as bacterial, viral, yeast, parasitic and fragal infections, and cancer. These compositions act by inhibiting funcal infections of pathogens, or cancer cells. One of the prophylactic applications of the ligand/receptor specificity exchangers includes coating or crosslinking it to a medical device or implant which include number of bacterial species. Abd2831-ABG6282 represent ligand/receptor cancer calls.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel ligand/receptor specificity exchanger that redirects antibodies to receptors on pathogen or tumor cell, has specificity domain having ligand for receptor, and antigenic domain having epitope of pathogen or toxin.
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                                                                                                                                                                          Ligand/receptor specificity exchanger, antibody, pathogen receptor; bacterial infection, cancer; baraterial infection, cancer; parasitic infection, fungal infection, proliferation, antibacterial; virucide, cytostatic, antifungal; ligand/receptor specificity domain.
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                                                                                            Ligand/receptor specificity domain #41.
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(first entry)
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The present invention relates to ligand/receptor specificity exchangers comprising at least one specificity domain comprising a ligand for a receptor, and at least one antigenic domain joined to the specificity domain, where the antigenic domain comprises an epitope of a pathogen or toxin. The ligand/receptor specificity exchangers redirect antibodies to teceptors present on pathogens. They are useful for preventing and treating human diseases such as bacterial, viral, yeast, parastic and treating human diseases such as bacterial, viral, yeast, parastic and fungal infections, and cancer. These compositions act by inhibiting proliferation of pathogens, or cancer cells. One of the prophylactic applications of the ligand/receptor specificity exchangers includes coating or crosslinking it to a medical device or implant which include implantable medical devices that tend to serve as foci for infection by a number of bacterial species. Abd622915 and Abd62945-Abg62954 represent ligand/receptor specificity exchanger peptides used in the methods of the present invention
                                                                                                                                                                                                                                                                                                                                                          Novel ligand/receptor apecificity exchanger that redirects antibodies to receptors on pathogen or tumor cell, has specificity domain having ligand for receptor, and antigenic domain having epitope of pathogen or toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 58; DB 5; Length 27;
Pred. No. 0.04;
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 19; Page 24; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor specificity exchanger.
                                                                                                                                                                                 19-SEP-2000; 2000US-00664025
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                                                                                                                                     19-SEP-2001; 2001WO-IB002327
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Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                     Sallberg M, Flock J;
                                                                                                                                                                                                                                                                                                                  WPI; 2002-489707/52.
                                                                                                                                                                                                                         (TRIP-) TRIPEP AB.
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                                              WO200224887-A2.
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                                                                                           28-MAR-2002
    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADM74055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a new ligand specificity exchanger comprising a specificity domain comprising a ligand for a bacterial receptor and an antigenic domain joined to the specificity domain and comprising at least 5 and less than 200 consecutive amino acids of a protein from a pathogen or toxin. The ligand specificity exchanger is useful in preparing a composition for treating e.g., cancer or infections caused by virus, bacteria, parasite, fungus or yeast by redirecting existing antibodies to pathogens and cancer cells. This is the amino acid sequence of a ligand/receptor specificity exchanger specificity domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New ligand specificity exchanger comprising specificity or antigenic domain, useful in preparing a composition for treating e.g., cancer or infections caused by virus, bacteria, parasite, fungus or yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ligand/receptor specificity exchanger; antibody; pathogen receptor; bacterial infection; viral infection; yeast infection; cancer; parasitic infection; fungal infection; proliferation; antibacterial; virucide; cytoscatic; antibungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ligand/receptor specificity exchanger peptide #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 58; DB 8;
Pred. No. 0.029;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 41; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG62912 standard; peptide; 27 AA.
  exchanger
                                                                                                                                                                                                                                         27-DEC-1996; 96US-00737065.

08-FEB-1999; 99US-00246258.

21-MAR-2000; 2000US-00532106.

21-APR-2000; 2000US-0056605.

19-SEP-2000; 2000US-00664025.

19-SEP-2000; 2000US-00664955.

19-ARR-2001; 2001US-00839447.
                                                                                                                                                                                                                                                                                                                                                                                                                           19-SEP-2001; 2001WO-IB002327.
21-MAY-2002; 2002US-00153271.
30-AUG-2002; 2002US-00234579.
                                                                                                                                                                             21-FEB-2003; 2003US-00372735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||:| :||| ||
WYSMKKTTMKIIPF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sallberg M, Flock J;
receptor specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-022083/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SALL/) SALLBERG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 10; Conserv
                                                                                      US2003225251-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FLOC/) FLOCK J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                               19-APR-2001; 2
20-APR-2001; 2
19-SEP-2001; 2
                                                                                                                                  04-DEC-2003
                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG62912;
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RESULT 40

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Gaps

us-09-487-790a-1.rag

(SALL/) (FLOC/)

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A peptide with the SQ in AAP40614 is claimed together with peptides which comprise an AA SQ intermediate between residues 1-38 and 34-38 of AAP40614, e.g. see FT. (Updated on 16-AUG-2002 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant collagen-like polymers - useful for making gels, films,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a unnatural collagen-like polymer of the
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                        - useful as
                                                                                                                                                                                                                                                                                                                                                                                       Score 58; DB 1; Length 38;
Pred. No. 0.058;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collagen-like polymer; synthetic polymer; fibre coating;
                                                                                                                                                                                                     Peptide(s) isolated from fibrinogen Fragment Dianticoagulants and as thrombus imaging agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prosthetic device; catalytic substance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 7; Col 53; 93pp; English
                                                                                                                                                                                                                                                       Claim 4; Col 14; 16pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86US-00927258.
87US-00114618.
88US-00269429.
90US-00609716.
91US-00791960.
                                                                                                                                                                                                                                                                                                                                                                                          50.0%;
                                      81US-00250173
                                                                      81US-00250173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-00642255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00577046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW57671 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||:| :|| ||
WYSMKKTTMKIIPF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferrari FA, Cappello J;
                                                                                                                                      Budzynski AZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collagen-like polymer.
                                                                                                       (RESE ) RESEARCH CORP
                                                                                                                                                                       WPI; 1984-170828/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-387004/33
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         Sequence 38 AA;
                                    02-APR-1981;
                                                                      02-APR-1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-1987;
09-NOV-1988;
06-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5773249-A
        19-JUN-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1991
05-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibres, etc
                                                                                                                                        Olexa SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW57671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROT-)
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW57671
        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a new ligand specificity exchanger comprising a specificity domain comprising a ligand for a bacterial receptor and an antigenic domain joined to the specificity domain and comprising at least 5 and less than 200 consecutive amino acids of a protein from a pathogen or toxin. The ligand specificity exchanger is useful in preparing a composition for treating e.g., cancer or infections caused by virus, bacteria, parasite, fungus or yeast by redirecting existing antibodies to pathogens and cancer cells. This is the amino acid sequence of a ligand/receptor specificity exchanger of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide inhibitor (PI) obtd. as a plasmin degradation prod. Di of fibrinogen.
                                                                                                                                                                                                                                                                                                                   New ligand specificity exchanger comprising specificity or antigenic domain, useful in preparing a composition for treating e.g., cancer or infections caused by virus, bacteria, parasite, fungus or yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Score 58; DB 8; Length 27; 71.4%; Pred. No. 0.04; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anticoagulant; blood clotting inhibitor; fibrin-binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "specifically claimed"
34. .38
/note= "specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12. .38
/note= "specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                       Example 7; SEQ ID NO 114; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP40614 standard; peptide; 38 AA.
27-DEC-1996; 96US-00737085.
08-FEB-1999; 99US-00246258.
21-MAR-2000; 2000US-00532106.
21-APR-2000; 2000US-00556605.
19-SEP-2000; 2000US-00664925.
19-SEP-2000; 200US-00664945.
19-APR-2001; 200US-00839466.
20-APR-2001; 200US-0083947.
21-MAY-2002; 200US-00153271.
30-AUG-2002; 2002US-00153271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WYSMKKTTMKIIPF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thrombus imaging agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                   Sallberg M, Flock J;
                                                                                                                                                                                                                                                                                    WPI; 2004-022083/02.
                                                                                                                                                                                                     SALLBERG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 34
                                                                                                                                                                                                                      FLOCK J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-2002
04-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US4455290-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP40614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Best Loc Matches

ઠ g AAP40614

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              admixed with other natural or synthetic polymers or coatings on fibres, films, labware or other surfaces, e.g. prosthetic devices. The polymers may be used for binding a wide variety of specific binding materials, as catalytic substances (where the amino acid sequence may specifically chelate a wide variety of elements), as purification media, composites, laminates or adhesives. They may also be combined with inorganic or organic materials such as carbon fibres, nylon fibres, nitrocellulose, etc., as flask coatings or in synthetic matrices for the growth and study of cells, as affinity columns or as supports for biological materials. The polymers have collagen-like properties, but may be easily expressed in micro-organisms in high efficiency. The new sequences can be tailored to give the desired properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The amino acid sequence of the protein polymer adhesion substrate (PPAS) 1-D monomer repear unit. The sequence comprises 2 repeats of the CLP 3.7 gane encoded sequence linked to the human fibrin PoLSITE sequence and the human fibrin-derived peptide 9.2 (ARR80116; comprising an altered C-terminal 17 amino acid from human fibrin) and used to produce the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pendent group; repeating unit; enzyme recognition site; sealant; fibrin; enzymatic cross-linking; biocompatible material; structural integrity; medical adhesive; wound closure; tissue repair; transglutaminase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein polymers comprising repeating units and sequences - capable of enzyme-catalysed covalent bond formation useful as a biocompatible material for wound closure and tissue repair.
 The products may be used as films, fibres, moulded objects
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein polymer adhesion substrate 1-D monomeric repeat unit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "human fibrin-derived peptide 93.4"
                                                                                                                                                                                                                                                                                  Score 58; DB 2; Length 73; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "human fibrin POLSITE"
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 48; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR80332 standard; protein; 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US002728.
                                                                                                                                                                                                                                                                              50.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-00205518
                                                                                                                                                                                                                                                                                                                                                     4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                        ||||:| :|| ||
WYSMKKTTMKIIPF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33. .53
/note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-320413/41.
                                                                                                                                                                                                                                                                                             Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ98715.
                                                                                                                                                                                                                                               Sequence 73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9523611-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cappello J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR80332;
                                                                                                                                                                                                                                                                                                                                                                                      35
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant protein polymers - containing naturally occurring repetitive units for crosslinking by enzymes, useful as medical adhesives and sealants, depots and matrices.
polymer adhesion substrate (PPAS) 1-D (AAR80333). The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein polymer adhesive substrate; PPAS1-C; sealant; wound healing; CLP 3.7; collagen; human.
                                                                                                                                                      .
0
                                                                                                                    DB 2; Length 75
                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                         Protein polymer adhesive substrate PPAS1-C monomer.
                                                                                                                  Score 58; DB 2;
Pred. No. 0.12;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58; DB 2,
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                        AAW49716 standard; protein; 75 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Col 29; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00397633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
71.4%;
                                                                                                                    50.0%;
71.4%;
                                                                                                                                                                                    4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                  Query Match
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                   35 WYSMKKTTMKIIPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-387091/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV32071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 75 AA;
                                                                                  Sequence 75 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
12-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5773577-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cappello J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                          AAW49716;
                                                                                                                                                                                                                                                                       RESULT 45
                                                                                                                                                                                                                                                                                        AAW49716
 8888888
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us-09-487-790a-1.rag

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WPI; 1995-320413/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 125 AA;
                                                                                                                                                                               WO9523611-A1
                                                                                                                                                                                                                       03-MAR-1995;
                                                                                                                                                                                                                                            03-MAR-1994;
                              18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1998
                                                                                                                                                                                                                                                                                     Cappello J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5773249-A
                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
           AAR80333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 48
                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW5767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potein polymer adhesive substrate PPASI-D monomer comprises human fibrin gamma POLSITE inserted into a structural backbone of collagen repeat motifs (see AAW4711). A PPASI-D polymer (see AAW49722) has been expressed in Escherichia coli HB101 transformants. Claimed recombinant protein polymers are capable of covalent crosslinking by enzymatic reaction to form products which set quickly and have good adhesive properties and high strength. CLP (collagen like protein) polymers are extremely soluble in water, allowing protein solutions of over 10 wt.% to be formed while maintaining good flow properties. CLP polymers have good adhesion to hydrophilic surfaces and therefore may adhere well to tissue. The fibrin PoLSITE confers the ability to polymerise adjacent fibrin molecules through thair specific interaction with the N-terminal residues of the fibrin alpha chain. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant protein polymers - containing naturally occurring repetitive units for crosslinking by enzymes, useful as medical adhesives and sealants, depots and matrices.
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                        Protein polymer adhesive substrate, PPAS1-D; sealant; wound healing; CLP 3.7; collagen; fibrin; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
Indels
                                                                                                                                                                   Protein polymer adhesive substrate PPAS1-D monomer.
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58; DB 2;
Pred. No. 0.12;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                        (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR80333
ID AAR80333 standard; protein; 125 AA.
                                                                                          AAW49721 standard; protein; 75 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Col 31; 70pp; English.
5
                                                                                                                                                                                                                                                                                                95US-00397633
                                                                                                                                                                                                                                                                                                                    94US-00205518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%;
71.4%;
                   4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 WYSMRKMSMKIRPF 17
                                                                                                                                               (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 WYSMKKTTMKIIPF
                                      35 WYSMKKTTMKIIPF
                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-387091/33.
                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV32073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 75 AA;
                                                                                                                                                                                                                     Synthetic.
Homo sapiens
                                                                                                                                                                                                                                                                                                                    03-MAR-1994;
                                                                                                                                                                                                                                                                                                02-MAR-1995;
                                                                                                                                     25-MAR-2003
12-OCT-1998
                                                                                                                                                                                                                                                      US5773577-A.
                                                                                                                                                                                                                                                                           30-JUN-1998
10;
                                                                                                                                                                                                                                                                                                                                                              Cappello J;
                                                                                                                AAW49721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 47
                                                                                AAW49721
                                                                                                                원
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Pendent group, repeating unit, enzyme recognition site; sealant, fibrin, enzymatic cross-linking, biocompatible material; structural integrity; medical adhesive; wound closure; tissue repair; transglutaminase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The amino acid sequence of the protein polymeric adhesion substrate (PPAS) 1-D. The protein comprises 2-20 repeats of the PPAS1-D monomeric repeat (AAR80312) which consists of the CLP 3.7 gene encoded sequence (AAR8031) linked to the human fibrin POLSITE sequence and the human fibrin cross-linking substrate peptide 93.2 sequence (AAR80316). The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein polymers comprising repeating units and sequences - capable of enzyme-catalysed covalent bond formation useful as a biocompatible material for wound closure and tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 34. .107
/note= "this sequence may be repeat 2-20 times"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collagen-like polymer; synthetic polymer; fibre coating; prosthetic device; catalytic substance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%; Score 58; DB 2; 71.4%; Pred. No. 0.21; iive 2; Mismatches
                                                                      Protein polymeric adhesion substrate 1-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 49; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW57672 standard; peptide; 198 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-US002728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-00205518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 71.4%;
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen-like polymer.
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Protein polymer adhesive substrate PPAS1-D comprises multiple repeats of a monomer (see AAW49721) consisting of human fibrin POLSITE inserted into a structural backbone of collagen repeat motifs (see AAW49711). The PPAS1-D polymer has been expressed in Escherichia coli HB101 transformants. Claimed recombinant protein polymers are capable of covalent crosslinking by enzymatic reaction to form products which set quickly and have good adhesive properties and high strength. CLP (collagen like protein) polymers are extremely soluble in water, allowing protein solutions of over 10 wt.* to be formed while maintaining good flow properties. CLP polymers have good adhesion to hydrophilic surfaces and therefore may adhere well to tissue. The fibrin FOLSITE confers the ability to polymerise adjacent fibrin molecules through their specific interaction with the N-terminal residues of the fibrin alpha chain. (Updated on 25-
                                                                                                                                                                                                                           New recombinant protein polymers - containing naturally occurring repetitive units for crosslinking by enzymes, useful as medical adhesives and sealants, depots and matrices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatic parenchymal cell growth factor; HPGF; liver diseases;
liver cancer; cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58; DB 2; Length 198;
Pred. No. 0.34;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat hepatic parenchymal cell growth factor.
                                                                                                            (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .24
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR65759 standard; protein; 314 AA.
                                                                                                                                                                                                                                                                                                          Example 5; Col 31; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAR-2003 to correct PF field.)
                                    95US-00397633.
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                                                                        94US-00205518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||:|:|||||
68 WYSMKKTTMKIIPF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                         WPI; 1998-387091/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9421678-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-1993;
                                    02-MAR-1995;
                                                                        03-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
17-MAY-1995
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30-JUN-1998
                                                                                                                                                 Cappello J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR65759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 50
AAR65759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a unnatural collagen-like polymer of the invention. The products may be used as films, fibres, moulded objects and admixed with other natural or synthetic polymers or coatings on fibres, films, labware or other surfaces, e.g. proethetic devices. The polymers may be used for binding a wide variety of specific binding materials, as catalytic substances (where the amino acid sequence may specifically chelate a wide variety of elements), as purification media, composites, laminates or adhesives. They may also be combined with inorganic or organic materials such as carbon fibres, nylon fibres, infrocellulose, etc., as flask coatings or in synthetic matrices for the growth and study of cells, as affinity columns or as supports for biological materials. The polymers have collagen-like properties, but may be easily expressed in micro-organisms in high efficiency. The new sequences can be tailored to give the desired properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein polymer adhesive substrate, PPAS1-D; sealant; wound healing; CLP 3.7; collagen; fibrin; human.
                                                                                                                                                                                                                                                                                                                                                              Recombinant collagen-like polymers - useful for making gels, films,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
34. .179
/note= "PPAS1-D monomer, repeated 2-20 times"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein polymer adhesive substrate PPAS1-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                               (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW49722 standard; protein; 198 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           Example 7; Col 57; 93pp; English
                                                                                                      870S-00114528
88US-00269429
90US-00609716.
91US-00791960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%;
71.4%;
                                                    96US-00642255
                                                                                          86US-00927258
                                                                                                                                                                                                         95US-00577046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||:| :||| || 68 WYSMKKTTMKIIPF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4
Matches 10, Conservative
                                                                                                                                                                                                                                                                                  Ferrari FA, Cappello J;
                                                                                                                                                                                                                                                                                                                        WPI; 1998-387004/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                        04-NOV-1986;
29-OCT-1987;
09-NOV-1988;
                                                                                                                                               06-NOV-1990;
12-NOV-1991;
05-NOV-1992;
                                                  02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                      fibres, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
12-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5773577-A.
            30-JUN-1998
                                                                                                                                                                                                         22-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW49722;
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RESULT 49 AAW49722

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Gaps .. 0

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Hara H, Yoshimura H, Matsuki Y, Shindo S, Hanada K;
           WPI; 1994-316940/39.
N-PSDB; AAQ77818.
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Hepatic parenchymal cell growth promoter peptide - is isolated from human or animal liver cell or produced by recombinant techniques and used for therapy of liver diseases.
                                                                                                                                                                                                                                   AAQ77818 encodes AAR65759 rat hepatic parenchymal cell growth factor (HPGF). The protein or the N-terminal peptide (AAR65758) may be used in the diagnosis and treatment of liver diseases, such as liver cancer and cirrhosis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.0%; Score 58; DB 2; Length 314; Best Local Similarity 52.4%; Pred. No. 0.55; Matches 11; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KGSWYSMRKMSMKIRP--FFP 19
                                                                                                                                                         Claim 3; Page 34; 47pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
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1;

Search completed: January 18, 2005, 11:10:45 Job time : 156 secs

:| |||::: ||||| | | 291 RGWWYSLKSVVMKIRPSDFIP 311

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                Copyright
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- protein search, using sw model OM protein Run on:

January 18, 2005, 11:04:00 ; Search time 39 Seconds (without alignments) 51.809 Million cell updates/sec

US-09-487-790A-1 116 1 KGSWYSMRKMSMKIRPFFPQQ 21 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 65 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	beta-fibrinogen -	fibrinogen beta ch		beta	beta	fibrinogen beta ch	fibrinogen gamma-A		1	fibrinogen gamma-A					androgen receptor	conserved hypothet	hypothetical prote	hypothetical prote	ein	probable transposa		hypothetical prote	probable transposa			receptor kinase ho	transcription init		
SUMMARIES	CI (167595	FGHUB	A05299	FGBOB	A38463	A25052	FGHUG	FGHUGB	JN0596	FGRTGA	805313	FGRTGB	A32670	D44234	G01627	B64420	F71003	E70562	VGBE37	F75550	C75533	E71188	E75452	G75376	JC8027	T04108	C69218	G69282	A75531
	DB	7	Н	7	7	~	7	ч	н	~	-	~	-	7	~	~	Н	N	N	Н	~	~	N	~	7	7	~	7	Н	~
	Length	55	491	328	468	463	479	437	453	312	437	444	445	438	998	716	128	125	115	841	409	486	399	408	40	4		٣	490	598
d e	Query	100.0	100.0	91.4	œ,	83.6	_	•	_	48.3	48.3		48.3	44.0	44.0	42.2	40.9	40.5	v	39.7	38.8		٠	٠	37.9	37.9	37.9	37.1	37.1	
	Score		116	106	103	97	83	9	9	26	99	26		51	21	4	47.5	47	46	46	45	44.5	44	44	44	44	44	43	43	43
	Result No.	-	7	٣	4	S	ø	7	80	σ	10	11	12		14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

hypothetical prote hypothetical prote hypothetical prote cyclin B - African RNA-directed RNA p probable signa 54 probable signa 54 probable signa 64 hypothetical prote 195 proteosome sub fibrinogen gamma c probable aldehyde hypothetical prote hypothetical prote conjugal transfer probable membrane conjugal transfer probable membrane probable membrane probable membrane conserved hypothet endoplasmic reticu heterodisulfide re hypothetical prote conserved hypothet conserved hypothet conserved hypothet hypothetical prote	probable serine/th cobyric acid synth tungeten-containin probable large gly peptidyl-dipeptida peptidyl-dipeptida tenascin - African
T27431 H69933 C9957 T00133 C91339 C91514 T42242 T42242 T42033 FGLMGS F71094 T114080 AB3186 S57163 S57163 S57163 S57163 S57163 S57163 S57163 S57163 S57163 S57163 S57163 S57163 S57163 S57163 S7	T05270 AD3338 B75071 A36105 A34171 I51647
2	50 50 60 177 131 131
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ALIGNMENTS

lefasion rat (fragment)

beta-fibrinogen - rat (fragment)

c;Species: Rattue norvegicus (Norway rat)

c;Species: Rattue norvegicus (Norway rat)

c;Accession: 167595

R;Sobczak, J; Lotti, A.

Lefas, A.

A;Title: Molecular cloning of mRNA sequences transiently induced during rat liver regen A;Reference number: 153408; MUID:87134033; PMID:3817019

A;Reference number: 153408; MUID:87134033; PMID:3817019

A;Reference number: 1555 KBS.

A;Recassion: 167595

A;Retus: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-55 kBS.

A;Coss-references: UNIPROT:P14480; GB:M35602; NID:g204141; PIDN:AAA41159.1; PID:g20414

C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf
F;1-51/Domain: fibrinogen beta/gamma homology (fragment) <FBG>

Query Match
100.0%; Score 116; DB 2; Length 5
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 35 KGSWYSMRKMSMKIRPFFPQQ 55 21 1 KGSWYSMRKMSMKIRPFFPQQ ઠે

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Gaps

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Length 55;

RESULT 2

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fibrinogen beta chain precursor [validated] - human N;Alternate names: coagulation factor I N;Contains: fibrinopeptide B

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Arithe: The structures of fibringen and fibrin.

Arithe: R.F.

Annu. Rev. Biochem. 53, 195-229, 1984

Arithe: Fibringen and fibrin.

Arithe: Fibringen and fibrin.

Arithe: Structures of fibringen and fibrin.

Arithe: Arcad. Sci. 408041; MUID: 84305751; PMID: 6383194

Arithe: Choning of fibringen genes and their cDNA.

Ann. N. Y. Acad. Sci. 408, 449-456, 1980

Arithe: Cloning of fibringen genes and their cDNA.

Arithe: Cloning of fibringen genes and their cDNA.

Arithe: Choning of fibringen genes and their cDNA.

Arithe: Choning of fibringen genes and their cDNA.

Arithe: Annotation

Rikirschbaum, N.E.; Budzynski, A.Z.

Arithe: A unique protecolytic fragment of human fibringen containing the Aalpha COOH-target annotation; hementin cleavage site

Arithe: A unique protecolytic fragment of human fibringen containing the Aalpha COOH-target annotation; hementin cleavage site

Arithe: A unique protesse from Haementeria ghiliani; the giant South American leech comment: The conversion of fibringen to fibrin is triggered by thrombin, which cleav conversion sites responsible for the formation of the soft clot.

Cromment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabil) conversion.

Cromment: All fibringen chains are synthesized in the liver.
     in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Fol
A,Title: The structures of fibrinogen and fibrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KGSWYSMRKMSMKIRPFFPQQ
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A; Residues: 164-174 < kUN>
A; Note: identification of tryptic peptides from high-density lipoproteins
A; Note: identification of tryptic peptides from high-density lipoproteins
B; Henschen, A; Lottspeich, F; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A; Title: Covalent structure of fibrinogen.
A; Reference number: A90037; MULD: 8255689
A; Contents: annotation; review, disulfide bonds
R; Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.
R; Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.
A; Contents: J. Biochem. 77, 595-610, 1977
A; Title: Primary structure of human fibrinogen. Characterization of disulfide-containing A; Reference number: A91249; MULD: 774599; PMID: 891553
A; Contents: annotation; disulfide bonds
R; Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G
                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 9-191, P', 193-491 <CHU>
A; Cross-teneces: UNIPROT: P02675
B; Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davie, E.W.
Biochemistry 22, 3244-3250, 1983
A; Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyribonu
A; Reference number: A90469; MUID: 83283433; PMID: 6688356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Molecule type: Lary, E, 114-137, OS', 140-144, OP', 147-148 <BLO>
A; Residues: 31-112, E', 114-137, OS', 140-144, OP', 147-148 <BLO>
B; R; Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A; Title: Identification of proteins associated with apolipoprotein A-I-containing lipopx A; Reference number: A54223; MUID:94162201; PMID:8117655
A; Accession: G54223
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence revision 31-Mar-1993 #text change 09-Jul-2004
C;Date: 24-Apr-1984 #sequence revision 31-Mar-1993 #text change 09-Jul-2004
C;Accession: B43256; A90469; E90469; E90463; A94433; A90437; A94309; G54223; A03121; B37
R;Chung, D.W.; Harris, J.E.; Davite, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A;Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A;Reference number: A43568; MUID:91344740; PMID:2102623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mENA
A; Residues: 9-191, 'A', 193-491 < CH2>
A; Cross **references: GB: 200129; NID: 9182429; PIDN: AAA52429.1; PID: 9182430
B; Huber, P.; Dalmon, J.; Cuttois, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
Nucleic Acids Res. 15, 1615-1625, 1987
A; Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene.
A; Reference number: 137389; MUID: 87146483; PMID: 3029722
A; Accession: 137389
A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Molecule type: DNA
A, Residues: 1-38 < HUBS.
A, Cross-references: BMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
B, Henschen, A.; Lottspelch, F.; Southan, C.; Topfer-Petersen, E.
in Protides of the Biological Fluids, Proc. 28th Collog., Peeters, H., ed., pp.51-56, PA, Title: Human fibrinogen: Bequence, sulfur bridges, glycosylation and some structural A, Reference number: A94433
A, Contents: carbohydrate binding
A, Accession: A94433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Accession: A90437
A.Molecule type: protein
A.Residues: 31.144, QP., 147-231, D,,233-330, E,,332-491 <WAT>
A.Residues: 31.144, QP., 147-231, D,,233-330, E,,332-491 <WAT>
R.Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A.Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A.Reference number: A94309; MUID:76225080; PMID:936108
A.Accession: A94309
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                                                                                                                                                                                                                                                                                                                                                    A; Accession: B43568
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A;Map position: 4q28-4q28
A;Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FC
ins are contained in the core. Two three-chain coiled coils emerge from this core and co
from the distal domain nodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; DesCipture: Intilingen Creaved by circumating years monomore and programme to the parkingly: blood coagulation coiled coil; glycoprotein; liver; plasma; pyroglutamic ac C; Superfamily: fibrinogen beta chain; fibrinogen beta chain sequence #status predicted <SIG> C; Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglutamic ac F; 1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG> F; 1-44/Product: fibrinogen beta chain #status experimental <APT> F; 31-44/Product: fibrinogen beta chain #status experimental <APT> F; 545-49/Product: fibrinogen disulfide ring homology <FDR> F; 59-228/Domain: fibrinogen beta/gamma homology <FDR> F; 518-487/Domain: fibrinogen beta/gamma homology <FBR> F; 314-44/S/Cleavage site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment F; 44-45/Cleavage site: Arg-Gly (thrombin) #status experimental F; 106/Disulfide bonds: interchain (to alpha-65) #status experimental F; 110/Disulfide bonds: interchain (to alpha-184) #status experimental F; 222/Disulfide bonds: interchain (to alpha-184) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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N;Contains: fibrinopeptide B
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jun-1987 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: A06299; PB0010
C;Accession: Mullio, N.T.; Comeau, C.M.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 81, 2313-2316, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;394/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 116; DB 1; Length 491; 100.0%; Pred. No. 9.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231-316,241-270,424-437/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
C,Genetics:
A,Gene: GDB:FGB
A,Cross-references: GDB:119130; OMIM:134830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGSWYSMRKMSMKIRPFFPQQ 491
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Gaps

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468;

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C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf C; Keywords: blood coagulation; glycoprotein; plasma; pyroglutamic acid; sulfoprotein p; 76-205/Domain: fibrinogen disulfide ring homology <FBR>
F; 215-464/Domain: fibrinogen beta/gamma homology <FBR>
F; 215-464/Domain: fibrinogen beta/gamma homology <FBR>
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F; 6/Binding site: sulfate (Tyr) (covalent) #status experimental F; 21-22/Cleavage site: Arg-Gly (thrombin) #status experimental F; 371/Binding site: carbohydrate (Apr) (covalent) #status predicted F; 372-373/Cleavage site: Arg-Thr (plasmin) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibringen beta chain - sea lamprey (fragments)
N; Contains: fibrinopeptide B
N; Contains: fibrinopeptide B
C; Spece Etcomyzon marinus (sea lamprey)
C; Date: 25-Oct.1987 #sequence revision 19-Peb-1999 #text_change 09-Jul-2004
C; Accession: A55052; A03124; B03124
R; Bohonus, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
Biochemistry 25, 6512-6516, 1986
A; Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A; Reference number: A25052; MUID:87076582; PMID:3790537
A; Molecule type: mRNA
A; Residues: 39-479 < ABOH>
A; Residues: 39-479 < ABOH>
A; Cross-references: UNIPROT: P02678; GB:M14773; NID:G213191; PIDN:AAA49261.1; PID:G21319
R; Cottrell, B.A.; Doolittle, R.F.
R; Cottrell, B.A.; Doolittle, R.F.
Biochim: Biophys: Acta 453, 426-438, 1976
A; Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization of A; Accession: A, A, Accession: A, Accession: A, A, Accession: A, Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A03124
A;Molecule type: protein
A;Recidues: 1-36 <COTI>
A;Accession: B03124
A;Accession: protein
A;Recidues: 37-42 <COT2>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an atypical thrombin cleavage si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
Cispecession: A38463.
Cispecies: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
Cispecession: A38463, 1991
A;Reference number: A38463; MUID:91182745; PMID:2009266
A;Reference number: A38463; MUID:91182745; PMID:2009266
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 103; DB 1;
Pred. No. 1.2e-08;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 97; DB 2; Pred. No. 1.1e-07; 3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fibrinogen beta chain - chicken (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KGSWYSMRKMSMKIRPFFPQQ 21
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81.0%;
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Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
Matches 16; Conserv
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A; Residues: 1-463 <WEI>
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A, Residues: 1-32 < FONA
A, Residues: 1-32 < FONA
A, Residues: 1-32 < FONA
A, Cross-references: UNIPROT: P14480
A, Title: Cloning and characterization of a CDNA for the B beta chain of rat fibrinogen:
A, Accession: PE0010
A, MUID: 89378771; PMID: 2673932
A, Accession: PE0010
A, MOlecule type: MRNA
A, Molecule type: MRNA
A, Residues: 33-328 < EAS>
A, Cross-references: GB: MA7220; NID: 9529585; PIDN: AA41160.1; PID: 9529586
C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfit
C; Superfamily: fibrinogen disulfide ring homology (fregment)
F; 33-65/Domain: fibrinogen beta/gamma homology (Fregment)
F; 73-124/Domain: fibrinogen beta/gamma homology RBG>
F; 731/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Residues: 373-374 <MED>
C,Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
C,Comment: Pibrinogen is a hexamer containing two sets of three nonidentical chains (alp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
A;Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
A;Reference number: A37513; MUID:81199473; PMID:6262803
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Accession: A05299 AUID:84194000; PMID:6232608
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A;Residues: 5-21 <530>
R;Martinelli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach,
Arch. Biochem. Biophys. 192, 27-32, 1979
A;Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrir
A;Reference number: A37507; MUID:79164394; PMID:434821
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R;Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
PEBS Lett. 23. 56-60, 1988
A;Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment
A;Reference number: S02443; MUID:88211875; PMID:2966748
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N;Contains: fibrinopeptide B
C;Species: Bos primigenius taurus (cattle)
C;Date: 29-Jul-1981 #sequence revision 29-Jul-1981 #tex
C;Accession: A03122, B03117; B37507; A37513; S02443
R;Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A;Tile: The sequence of amino acids at the N-terminal of Reference number: A03122
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A;Residues: 1-4 <BLO>
R;Sjoquist, J:; Blomback, B.; Wallen, P.
Ark. Kemi 16, 425-436, 1960
A;Tele: Amino acid sequence of bovine fibrinopeptides.
A;Reference number: A03117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 106; DB 2;
Pred. No. 2.7e-09;
1; Mismatches 1;
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Best Local Similarity 90.5'
Matches 19; Conservative
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A; Residues: 22-53 <MAR>
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PIDN:AAA48770.1; PID:g21178 homology; fibrinogen disulf

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Gaps

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A; Reference number: A40698; MUID:93286185; PMID:8509453
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A,Residues: 209-270 <RES>
A/Cross-references: BMBLX00086; NID:g31445; PIDN:CAA24944.1; PID:g577055
R;Bertagnoll: M.E.; Beckerle, M.C.
J. Cell Biol. 121, 1329-1342, 1993
A;Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with th
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A;Molecule type: protein
R;Residues: 27-437 <HRN:
R;Kant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
A;Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains: ev
A;Reference number: A93956; MUID:83247396; PMID:6575389
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*Residues: 276-437 <KNN>

*R. Residues: 276-437 <KNN>

*R. Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.

J. Biol. Chem. 259, 12826-12830, 1984

J. Biol. Chem. 259, 12826-12830, 1984

J. Fitle: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the A; Reference number: A92448; MUID:85030379; PMID:6092346
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A; Residues: 286-437 <FOR>
R; Ramidues: 286-437 <FOR>
Nucleic Acids Res. 11, 7427-7434, 1983
Nucleic Acids Res. 11, 7427-7434, 1983
A; Title: Isolation and characterisation of cDNA clones for the Aalpha- and gamma-chains A; Reference number: I37393; MUID:84069777; PMID:6689067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Date: 24-Apr-1984 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
(Accession: A90470; B90494; C94433; B93956; B92448; I37393; A40698; H54223; A03125; C376hung, D.W.; Chan, W.Y.; Davide, E.W.
(Johnelistry 22, 3250-3256, 1983)
(Fight : Characterization of a complementary deoxyribonucleic acid coding for the gamma; Reference number: A90470; MUID:83283434; PMID:6688357
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A; Residues: 1-113,'1', 115-437 <RIX>
A; Residues: 1-113,'1', 115-437 <RIX>
A; Cross-references: GB:X02415; GB:M10014; NID:g182438; PIDN:AAB59531.1; PID:g182439
B; Hennachen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
in Protides of the Biological Fluids, Proc. 28th Collog., Peeters, H., ed., pp.51-56, PA; Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural A; Reference number: A94433
A; Accession: C94433
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Biochemistry 24, 2077-2086, 1985
A.Yitle: Nuclectide sequence of the gene for the gamma chain of human fibrinogen.
A.Reference number: A90494; MUID:85252774; PMID:2990550
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C; Keywords: blood coagulation; glycoprotein; sulfoprotein
F;1-36/Product: fibrinopeptide # #status experimental <FPB>-
F;37-479/Product: fibrinopen chain #status experimental <MAT>-
F;90-219/Domain: fibrinogen disulfide ring homology <FDR>-
F;229-477/Domain: fibrinogen beta/gamma homology <FBG>-
F;121/Binding site: sulfate (Tyr) (covalent) #status experimental
F;27/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Best Local Similarity 73.7%; Pred. No. 1.9e-05;
Matches 14; Conservative 4; Mismatches 1; Indels
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A; Residues: 1-437 < CHU>
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A Molecule type: protein

A, Residues: 27-33, XX, 36-41 < BER>
A, Note: sequence extracted from NCBI backbone (NCBIP:133734)

R, Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.

B, Chemistry 33, 1988-1993, 1994

A, Title: Identification of proteins associated with apolipoprotein A-I-containing lipops
A, Reference number: A54223, MUID:94162201; PMID:8117655
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A; Residues: 27-33, 'XX', 36-41 < KUN>
A; Residues: 27-33, 'XX', 36-41 < KUN>
A; Rote: identification of tryptic peptides from high-density lipoproteins
A; Rote: identification of tryptic peptides from high-density lipoproteins
A; Tottes (Covalent structure of fibrinogen.
A; Title: Covalent structure of fibrinogen.
A; Reference number: A90037; MUID: 83254370; PMID: 6575689
A; Contents: annotation; review, disulfide bounds
A; Reference number: A94437
A; Reference number: A9430; MUID: 76225080; PMID: 936108
A; Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A; Reference number: A94309; MUID: 76225080; PMID: 936108
A; Contents: annotation; disulfide bounds
A; Reference number: A94309; MUID: 76225080; PMID: 93608
A; Title: Disulfide bridges in NH-2-terminal part of human fibrinogen are joined through disulfide bonds
A; Reference number: A94309; MUID: 83231465; PMID: 6860649
A; Reference number: A90467; MUID: 83231465; PMID: 6860649
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Annu. Rev. Biochem. 53, 195-229, 1984

AjTitle: Fibringon and fibrin.

AjReference number: A90041; MUID: 84305751; PMID: 6383194

AjContents: annotation; review, EM structure, polymerization, ligands

AjContents: annotation; review, EM structure, polymerization, ligands

Ridorwitz, B.H.; Varadi, A.; Scheraga, H.A.

Proc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984

AjTitle: Localization of a fibrin gamma-chain polymerization site within segment Thr-374

AjContents: annotation; polymerization region

Rikloczewiak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.

Biochemistry 23, 1767-1774, 1984

AjTitle: Datellet receptor recognition site on human fibrinogen. Synthesis and structure
AjReference number: A90483; MUID:84203545; PMID:6326808

AjTitle: Datellet receptor recognition site on human fibrinogen. Synthesis and structure
AjReference number: A90483; MUID:8418664; PMID:6326808

AjTitle: Evidence that three adhesive proteins interact with a common recognition site of AjReference number: A92477; MUID:8418564; PMID:6326305

AjTitle: Exidence that three adhesive proteins interact with a common recognition site of AjReference number: A92497; MUID:8418664; PMID:6326305

AjTitle: Localization of a fibrinogen calcium binding site between gamma-subunit position
AjReference number: A92249; MUID:85261382; PMID:3160702

AjContents: annotation; calcium binding region
Rikinschbaum, N.E.; Budzynski, A.Z.

Aj Biol. Chem. 265, 13676-1390
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A,Reference number: A37117; MUID:90337977; PMID:2143188
A,Contents: annotation; hementin cleavage site
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C,Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabil) ger) and between alpha chains (weaker) of different monomers.
C,Comment: All fibrinogen chains are synthesized in the liver.
C,Comment: The two forms of gamma chain, A and B (see PIR:FGHUGB), arise by alternate sgintron, which makes this chain different from the gamma-B chain at positions 434-437 and C,Genetics:
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 75-286 <RES.
A;Cross-references: EMBL:X51473; NID:g31410; PIDN:CAA35837.1; PID:g930064
C;Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate up ntron, which makes this chain different from the gamma-B chain at positions 434-437 and C;Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 4q28-4q28
A;Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:F ins are contained in the core. Two three-chain coiled coils emerge from this core and c from the distal domain nodes.
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C; Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C; Reywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein
C; Superfamily: fibrinogen gamma chain #status predicted <SIG>
C; Keywords: alternative splicing; blood coagulation; coiled coil; glycoprotein
C; Superfamil: signal sequence #status predicted <SIG>
F; 27-45; Droduct: fibrinogen peta/gamma-B chain #status experimental <MPT>
F; 176-415; Domain: fibrinogen beta/gamma homology <FIGS>
F; 310-325; Region: polymerization site, binding to the amino end of the alpha chain of a F; 35/Disulfide bonds: interchain (to gamma-35) #status predicted
F; 35/Disulfide bonds: interchain (to beta-110) #status predicted
F; 49/Disulfide bonds: interchain (to alpha-64) #status predicted
F; 165/Disulfide bonds: interchain (to alpha-180) #status predicted
F; 165/Disulfide bonds: interchain (to alpha-180) #status predicted
F; 165/Disulfide bonds: interchain (to alpha-180) #status predicted
F; 179-208, 352-365/Disulfide bonds: #interchain to Lys-432 NG-amino) #status predicted
F; 177-Cross-link: isopeptide (Lys) (interchain to Gln-424) #status predicted
F; 177-Cross-link: isopeptide (Lys) (interchain to Gln-424) #status predicted
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A,Rebidues: 1-312 <YAN>
A,Rebidues: 1-312 <YAN>
A,Rebidues: 1-312 <YAN>
A,Reperances: Uniter type: mrn A,Experimental source: liver
F,1-17/Domain; signal sequence #status predicted <SIG>
F,18-312/Product: fibrinogen-related protein HFREP-1 #status predicted <MAT>
F,80-305/Domain: fibrinogen beta/gamma homology <FBG>
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C;Species: Home sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JNO596
R;Yamamoto, T.; Gotoh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Biochem: Biophys. Res. Commun. 193, 681-687, 1993
A;Title: Molecular cloning and initial characterization of a novel fibrinogen-related A;Reference number: JNO596; MUID:93290661; PMID:8390249
                                                  A Molecule type: protein
A;Residues: 433-453 cRR2-
R;Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A;Title: Polywacphism of the human gamma chain fibrinogen gene.
A;Reference number: 137390; MUID:92119334; PMID:1685103
A;Accession: 137390
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Pred. No. 0.09;
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A;Cross-references: GDB:119132; OMIM:134850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .7
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64.7%;
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                                                                                                                                                                                                                                                                                                                      A; Packribtion: fibrinogen cleaved by thrombin yields monomers that are polymerized into A; Packmay: blood coagulation
C; Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C; Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein;
C; Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein;
F; 1-26/Domain: signal sequence #status predicted <SIG>
F; 1-25/Domain: fibrinogen gamma-A chain #status experimental <MPT>
F; 10-415/Domain: calcium binding #status predicted <CAB>
F; 10-42/Region: polymerization site, binding to the amino end of the alpha chain of an F; 43-437/Region: polymerization site, binding to the amino end of the plane of F; 34-3-437/Region: polymerization site, binding to the amino end of the slpha chain of an F; 43-437/Region: polymerization site, binding to the amino end of the slpha chain interchain (to gamma-35) #status experimental
F; 35/Disulfide bonds: interchain (to gamma-35) #status experimental
F; 49/Disulfide bonds: interchain (to beta-110) #status experimental
F; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20; 10-20;
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A; Residues: 1-113, 17, 115-453 &RIX>
A; Residues: 1-113, 17, 115-453 &RIX>
A; Cross-references: UNIPROT: P02679; GB:M10014; GB:J00134; GB:J00135; GB:X00086; NID:g182
R; Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
A; Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the A; Reference number: A92448; MUID:85030379; PMID:6092346
A;Cross-references: GDB:119132; OMIM:134850
A;Map position: 4q28-4q28
A;Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3
A;Introns: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG ans are contained in the core. Two three-chain coiled coils emerge from this core and coffrom the distal domain nodes.
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A;Residues: 411-434, Y',436-440, Z',442, Z',444, B',446-447, R',449, ZBB',453 <WOL>
A;Residues: 411-434, Y',436-440, Z',442, Z',444, B',446-447, R',449, ZBB',453 <WOL>
A;Francia, C.W.; Mealler, E.; Henschen, B.; Simpson, P.J.; Marder, V.J.
Broc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A;Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-chain
A;Reference number: A24194; MUID:88217900; PMID:3368448
A;Accession: A28203
A;Molecule type: protein
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A; Mesidues: 286-453 < FOR>
R; Medifenstein-Todel, C.; Mosesson, M.W.
Biochemistry 20, 6146-6149, 1981
A; Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant
A; Meference number: A90453; MUID:82068993; PMID:7306501
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N;Alternate names: coagulation factor I; fibrinogen gamma-55 chain
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text change 09-Jul-2004
C;Accession: A90494; A92448; Ā90453; A28203; B28203; I37390; A03126
R;Rixon, M. W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A;Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
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KTRWYSMKKTTMKIIPF 415
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Best Local Similarity 64.7
Matches 11; Conservative
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Gaps

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CiSpecies: Rattue norregicus (Norway rat)
CiSpecies: Rattue norregicus (Norway rat)
CiAntes: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 27-Feb-1997
CiAccession: A03128; I58265
Ricrabtree, G.R.; Kant, J.A.
Ricrabtree, G.R.; Kant, J.A.
A;Title: Organization of the rat gamma-fibrinogen gene: alternative mRNA splice pattern: A;Reference number: A90828; MUID:83129318; PMID:6897622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-445 <CRA>
Kjancyan, J.G.; Holbrook, N.J.; Crabtree, G.R.
Nucleic Acids Res. 15, 2774-2776, 1987
A;Title: Nucleotide sequence of the gamma chain gene of rat fibrinogen: conserved intro
A;Reference number: 158265; MUID:87174801; PMID:3562236
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C;Comment: Gamma-B is formed from the same gene as gamma-A, probably as a result of fai'
C;Comment: The fibrinogen molecule is a hexamer containing two sets of three nonidentic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Speciës: Xenopus laevis (African clawed frog)
C,Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C,Accession: A33670; I53416
R;Pastori, R.L.; Moskaitis, J.E.; Smith Jr., L.H.; Schoenberg, D.R.
Biochemistry 29, 2599-2665, 1990
A;Title: Estrogen regulation of Xenopus laevis gamma-fibrinogen gene expression.
A;Reference number: A32670; MUID:90241882; PMID:2334684
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F;173-413/Domain: fibrinogen beta/gamma homology <FBG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology C;Keyworda: alternative splicing; blood coagulation; plasma F;1-25/Domain: signal sequence #status predicted <SIG>F;16-445/Product: fibrinogen gamma-B chain #status predicted <FGB>F;176-415/Domain: fibrinogen beta/gamma homology <FBG>
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XStatus: preliminary; translated from GB/EMBL/DDBJ
A;Aolecule type: DNA
A;Residues: 1-134 <RES>
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399 KTRWYSMKETTMKIIPF 415
                                              1 KGSWYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25/3; 41/3; 103/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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A,Molecule type: mRNA
A,Residues: 1-438 <PAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-58 < BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: I51416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A32670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A03128
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                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A90828; A93989; Ā03127
R;Crabtree, G.R.; Kant, J.A.
R;Crabtree, G.R.; Kant, J.A.
A;Title: Organization of the rat gamma-fibrinogen gene: alternative mRNA splice patterns A;Reference number: A90828; MUID:83129318; PMID:6897622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:K01337; NID:g204102; PIDN:AAA98626.1; PID:g204103
C;Comment: The fibrinogen molecule is a hexamer containing two sets of three nonidentica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S05313 K.M.; Foreman, R.C.; Saunders, N.R. N.P. Nucleic Acids Res. 17, 6397, 1989 A;Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibrind A;Reference number: S05313; MUID:89366676; PMID:2771651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Africestation of the ABO.

A.Residues: 1-44 < abo.

A.Residues: 1-444 < abo.

A.Residues: 1-444 < abo.

A.Cross-references: UNIPROT:P12799; EMBL:X15556; NID:g349; PIDN:CAA33562.1; PID:g350

A.Cross-references: UNIPROT:P12799; EMBL:X15556; NID:g349; PIDN:CAA33562.1; PID:g350

A.Note: the authors translated the codon AGT for residue 105 as Ala and ATT for residue C; Superfamily: fibrinogen gamma chain; fibrinogen betatus predicted <SIG>
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-444/Product: fibrinogen gamma-B chain #status predicted <MAT>

F;174-414/Domain: fibrinogen beta/gamma homology <FBG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Molecule type: mRNA
A Residues: 1-437 < CRA>
A Residues: 1-437 < CRA>
A Residues: 1-437 < CRA>
A Cross-references: UNIPROT: P02680

R FFOWLES, D.M.; Mullis, N.T.; Comeau, C.M.; Crabtree, G.R.
Proc. Natl. Acad. Sci. US.A. 81, 2313-2316, 1984
A Title: Potential basis for regulation of the coordinately expressed fibrinogen genes:
A Reference number: A93989; MUID:84194000; PMID:6232608
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology C; Keywords: alternative splicing; blood coagulation; plasma F;1-25, Domain: signal sequence #status predicted <SIG>F;26-437/Product: fibrinogen gamma-A chain #status predicted <FGA>F;176-415/Domain: fibrinogen beta/gamma homology <FGG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 437;
       Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.3%; Score 56; DB 1; 58.8%; Pred. No. 0.38;
       DB 2;
   Score 56; DB 2;
Pred. No. 0.27;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                          .brinogen gamma-A chain precursor - rat
                                                                                                                                                                              290 GWWYSLKSVVMKIRPNDFIP 309
                                                                                                                                   2 GSWYSMRKMSMKIRP--FFP 19
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Query Match
Best Local Similarity 55.0%;
Matches 11; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KGSWYSMRKMSMKIRPF
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Best Local Similarity 58.8
Matches 10; Conservative
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Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-102 < FOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Introns: 25/3; 41/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A93989
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                                                                                                                                                                                                                                                                                                          RESULT 10
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Conserved hypothetical protein MJ0962 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Accession: B64420
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R;Rult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.J.; Werbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi A;Reference number: A64300; MUD:96337999; PMID:8688087
A;Accession: B64420
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C;Accession: G01627
R;Bina, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                       Gaps
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F;686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                   Length 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Residues: 1-716 <BIN>
A, Cross-references: EMBL:U19345; NID:g726041; PID:g726042
                                                                Score 51; DB 2;
Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-716 <BIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, December 1994 A;Reference number: G07955 A;Accession: G01627
                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  androgen receptor 1 - human N;Alternate names: dihydrotestosterone receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: GDB:AR, DHTR, SBMA
A,Cross-references: GDB:120556, OMIM:313700
A,Map position: Xq11-Xq12
                                                                                                                                                                                                                                              1 KGSWYSMRKMSMKIRPFFPQ 20
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                                                            44.0%;
ilarity 50.0%;
Conservative
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Best Local Similarity
                                                            Query Match
Best Local Similarity
Matches 10; Conserv
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A; Residues: 1-128 <BUL>
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Best Local S
Matches 10
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F71003
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C; Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma C; Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein; F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
F; 30-863/Product: fibrinogen disulfide ring homology <FDR>
F; 57-185/Domain: fibrinogen disulfide ring homology <FDR>
F; 57-293/Region: cell attachment (R-G-D) motif
F; 52-863/Product: fibrinogen beta/gamma homology <FDR>
F; 22-460/Binding site: phosphate (Ser) (covalent) #status experimental
F; 52-460/Binding site: phosphate (Ser) (covalent) #status experimental
F; 55/Disulfide bonds: interchain (to alpha 47) #status experimental
F; 55/Disulfide bonds: interchain (to beta-95) #status experimental
F; 55/Disulfide bonds: interchain (to beta-95) #status experimental
F; 58/Disulfide bonds: interchain (to beta-166) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Notes estable 199e: mRNA, DNA
A, Residues: 605-866 <FU2>
A, Notes estable extracted from NCBI backbone (NCBIP:119917)
C, Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C, Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C, Comment: The seponsible for the formation of the soft clot.
C, Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliger) and between alpha chains (weaker) of different monomers.
C, Comment: All fibrinogen chains are synthesized in the liver.
C, Comment: See PIR: FGHUA for the major splice form. It is not known whether this form is
                                                                                                                                                                                                                                                                                                                                                                                                                                    NiAlternate names: coagulation factor I
NiContains: fibrinopeptide A
C;Species: Homo sapiens man)
C;Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: D44234; B44234
C;Accession: D44234; B44234
Biochemistry 31, 11968-11972, 1992
A;Title: Carboxy-terninal-extended variant of the human fibrinogen alpha subunit: a nove
A;Reference number: A44234; MUID:93090725; PMID:1457396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)Cross-references: GDB:119129; OMIM:134820
A;Map position: 4428-4428
A;Introns: 18/3; 60/3; 122/1; 171/2
A;Introns: 18/3; 60/3; 122/1; 171/2
A;Note: the list of introns is incomplete
C;Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentica ntained in the core. Two three-chain coiled coils emerge from this core and connect it the core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188,419/Binding site: carbohydrate (Asn) (covalent) #status absent
122/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
1347,385/Cross-link: 1sopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:P02671, GB:M58569; NID:g182406; PID:g182407
A;Note: neither the complete nucleic acid sequence nor the complete translation are show
A;Accession: B44234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;461-491/Disulfide bonds: #status experimenta.
F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status
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                                                                                                       Gaps
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                                                                                                       ö
                                   Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                           brinogen alpha chain precursor, extended splice form - human
                                                                                                   2, Indels
                            DB 2;
2.4;
                                                                                            3; Mismatches
                                Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA; DNA
A;Residues: 1-866 <FU1>
                            44.0%;
61.5%;
                                                                                                                                                                                                          ||||: ::||| |
400 WYSMKSVTMKIMP 412
                                                                                                                                                                4 WYSMRKMSMKIRP 16
                                                                                                Conservative
Query Match
Best Local Similarity
--hag 8; Conserve
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A,Cross-references: UNIPROT:P09260; EMBL:X04370; NID:g59989; PIDN:CAA27920.1; PID:g6002.
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Pred. No. 21;
4; Mismatches
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Pred. No. 30;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 1
C;Superfamily: hypothetical protein b1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 KATWYG--RLVSKISPYFP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KGSWYSMRKMSMKIRPFFP 19
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ilarity 42.1%;
Conservative
                                                                                                                                                                                      Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.4%;
Best Local Similarity 27.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                 5 YSMRKMSMKIRPFFP 19
                                                                                                                                                                                                                                                                                                                          Local Similarity
les 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-486 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: F75550
A;Status: preliminary
A;Molecule type: DNA
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A;Gene: DR0178
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Deolphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; WUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:O06371; GB:Z95436; GB:AL123456; NID:g3261770; PIDN:CAB08848.
A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                      R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi M.; Astitle: S. 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
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                                                                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence not shown; translation not shown
hypothetical protein PH1324 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug.1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein H - human herpesvirus 3
NyAlternate names: glycoprotein III
C;Species: human herpesvirus 3, varicella-zoster virus
C;Species: human herpesvirus 3, varicella-zoster virus
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C;Accession: B27341
R;Davison, AJ; Scott, J.E.
J; Gen. virul. 67, 1759-1816, 1986
A;Title: The complete DNA sequence of varicella-zoster virus.
A;Reference number: A27345; MUID:86306657; PMID:3018124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Mycobacterium tuberculosis
.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
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Pred. No. 4;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
40.5%; Score 47; DB
Best Local Similarity 42.1%; Pred. No. 3;
Matches 8; Conservative 5; Mismatches
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Best Local Similarity
Matches 8; Conserv
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A; Molecule type: DNA
A; Residues: 1-841 < DAV>
                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                C; Accession: F71003
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C;Genetics:
A;Gene: 37
C;Superfamily: herpesvirus glycoprotein H
C;Keywords: glycoprotein
F;18,45,83,217,317,499,522,560,760,783/Binding site: carbohydrate (Asn) (covalent) #sta
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A;Cross-references: UNIPROT:Q9RXX7; GB:AE001880; GB:AE000513; NID:g6457844; PIDN:AAF097
A;Experimental source: strain Rl
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C,Genetics:
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C;Species: Deinococcus radiodurans
C;Species: Decoccus radiodurans
C;Species: Decoccus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: C;Accession: J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable transposase - Deinococcus radiodurans (strain R1)
(Species Deinococcus radiodurans
(Species 103-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F7550
C;Accession: F7550
C;Accession: F7550
M: Shen, M: Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans in A;Reference number: A75250; MUID:20036896; PMID:10567266
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                                                                                                                                                                                                        Score 46; DB 1; Length 841;
Pred. No. 30;
3; Mismatches 4; Indels
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R.J.
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A,Residues: 1-408 «MH:»
A,Cross-references: UNIPROT:Q9RU04, GB:AE002003, GB:AE000513; NID:g6459358; PIDN:AAF111
A,Experimental source: strain R1
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T.; Zalewski,
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75376
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Vomter, J.C.; Fraser, C.M.
S; Smith, H.O.; Vomter, J.C.; Fraser, C.M.
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G73376
A;Status: Preliminary
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C;Accession: JC8027
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7
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larity 36.8%; Pred. No. 30;
Conservative 5; Mismatches
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Pred. No. 30;
5; Mismatches
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C,Superfamily: hypothetical protein b1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: hypothetical protein b1432
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310 KAAWYG--RLVSKVSPYFP 326
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310 KAAWYG--RLVSKVSPYFP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KGSWYSMRKMSMKIRPFFP 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: strain KD8301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.9%;
Best Local Similarity 36.8%;
Matches 7; Conservative
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-408 <WHI>
A;Cross-references: UNIPROT: 083029; GB:AE001950; GB:AE000513; NID:g6458699; PIDN:AAF1055
A;Experimental Bource: strain Rl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable transposase - Deinococcus radiodurans (strain R1)
Cispecies Deinococcus radiodurans
Cispecies Deinococcus radiodurans
Cispecies Benococcus radiodurans
F75369; G75335; F75401; D75492; T44372
F75369; G75335; F75401; D75492; T44372
F75369; G75335; F75401; D75492; T44372
F75369; M.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
Smith, H.O.; Venter, J.G.; Fraser, C.M.
Sismith, H.O.; Venter, J.C.; Fraser, C.M.
A; Santh, Benococcus radiodurans R1.
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Reference number: A75250; MUID: 20036896; PMID: 10567266
                                                                                                                                                                                                                                                                             R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi BINA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-408 <WH2>
A;Cross-references: GB:AE002064; GB:AE000513; NID:g6460134; PIDN:AAF11872.1; PID:g646013
A;Experimental source: strain R1
A;Accession: F75369
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-399 <KAW> A;Residues: 1-399 <KAW> A;Residues: UNIPROT:059446; GB:AP000007; NID:g3236134; PIDN:BAA30900.1; PID:g325
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| Cross-references: GB:AE002032, GB:AE000513; NID:g6459715, PIDN:AAF11486.1; PID:g645971
| Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Experimental source: strain OT3
A, Note: this accession replaces an interim accession for a sequence replaced by GenBank
C, Genetics:
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                                                                                                                                                                                  hypothetical protein PH1782 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: E71188
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                            | || : |: |
446 GQWYDLGKLSGWDHTAIVGIPGLQDVRPFYRNQ 478
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21
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Pred. No. 30;
6; Mismatches
--MKIRPFFPQQ
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A;Experimental source: strain R1
A;Accession: G75335
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45 GTWYLARKLSLELQ 58
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Best Local Similarity 42.9
Matches 6; Conservative
GSWYSMRKMS
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Residues: 1-408 <WH3>
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us-09-487-790a-1.rpr

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Gaps

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Nypothetical protein AF0263 - Archaeoglobus fulgidus
CiSpecies: 10-8p-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
CiAccession: G62282
EiXIENK, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.
Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaer
A;Accession: G62282
A;Status; preliminary; nucleic acid sequence not shown; translation not shown
                C, Superfamily: transcription initiation factor IIB; transcription initiation factor IIB
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hypothetical protein - Deinococcus radiodurans (strain R1)
c;Species: Deinococcus radiodurans
c;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
c;Accession: A7531
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, W.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
science 286, 1571-1577, 1999
A;Fitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RA;Fitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RA;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:029976; GB:AE001087; GB:AE000782; NID:g2689410; C;Superfamily: Aquifex aeolicus glucose-1-phosphate thymidylyltransferase
                                                       C,Keywords: duplication; transcription initiation
F;13-302/Domain: transcription initiation factor IIB homology <TF2B>
                                                                                                                                                                         37.1%; Score 43; DB 2; Length 310; 46.7%; Pred. No. 33; ive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.1%; Score 43; DB 1; Length 490; Best Local Similarity 47.4%; Pred. No. 53; Matches 9; Conservative 4; Mismatches 4; Indels
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Pred. No. 64;
5; Mismatches
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220 QGAWGQPPRMAPKLRPF 236
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99 RAQWYRLRKWQRKIR 113
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41.2%;
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Best Local Similarity 41.2
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-598 < WHI>
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A; Status: preliminary
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A,Map position: 1
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Ribecraft, P.W.; Stinard, P.S.; McCarty, D.R.

Science 273, 1406-1409, 1996

A;Title: CRINKIVA: A TNFR-like receptor kinase involved in maize epidermal differentiati

A;Reference number: 215216; MuID:96355669; PMID:8703079

A;Reference number: 215216; MuID:96355699; PMID:8703079

A;Residues: 1901 <BEC>

A;Rolecule type: mRNA

A;Nolecule type: mRNA

A;Residues: 1-901 <BEC>

A;Cross-references: UNIPROT:024585; EMBL:U67422; NID:g1597722; PIDN:AAB09771.1; PID:g159

C;Genetics:
R;Guo, D.F.; Chenier, I.; Tardif, V.; Orlov, S.N.; Inagami, T.
Biochem. Biophys. Res. Commun. 310, 1254-1265, 2003
A;Title: Type I angiotensin II receptor-associated protein ARAP1 binds and recycles the A;Reference number: JC8027; PMID: 14559250
A;Accession: JC8027
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-493 <GUO>
A;Cross-references: GB:AF159049
C;Comment: This protein, which interacts with the carboxyl terminal region of the ATIA respicially promotes the recycling of ATI receptor back to the plasma membrane after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cipecies: Methanobaccerium thermoutotrophicum (cipacies) Methanobaccerium thermoutotrophicum (cipacies) Methanobaccerium thermoutotrophicum (cipacies) Mechanobaccerium thermoutotrophicum (cipacies) Mechanobaccerium thermoutotrophicum (cipacies) Missains (cipacies) M
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C;Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprotein
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C;Species: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   C,Genetics:
A,Gene: arapl
C,Keywords: angiotensin II receptor; receptor recycling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.9%; Score 44; DB 2; 50.0%; Pred. No. 37;
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Pred. No. 67;
3; Mismatches
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472 RGGSYSLKKVVMMIRP 487
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| KSTAYSFRKDNMKIQP 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0
Matches 8; Conservative
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Best Local Similarity
Matches 9; Conserv
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A, Gene: MTH885
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Cyperacises: Mycobacterium tuberculosis: Cybertain Taylor (Species: Mycobacterium tuberculosis: Mycobacterium tuberculosis: Mycobacterium tuberculosis: Mycobacterium tuberculosis: Taylor, 17-101-1998 #text_change 09-Jul-2004 (Species: 17-Jul-1998 #text_change 09-Jul-2004 (Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004 (Species: 17-Jul-2004 #text_change 09-Jul-2004 #text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:007914; GB:Z95557; GB:AL123456; NID:g3242276; PIDN:CAB08948
A;Experimental source: strain H37Rv
A;Experimental source: strain H37Rv
A;Gene: Rv3618
C;Superfamily: alkanal monooxygenase [FMN-linked] (bacterial luciferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A56186

Yorlin E - African clawed frog
NyAlternate names: cyclin E1
NyAlternate names: cyclin E1
C;Species: Xenopus laevis (African clawed frog)
C;Species: Ashpr-1995 #sequence_revision 28-Apr-1995 #text_change 12-Jul-2004
C;Accession: A56186; S34125
R;Rempel, R.E.; Sleight, S.B.; Maller, J.L.
B101. Chem. 270, 6643-6855, 1995
A;Title: Maternal Xenopus Cdk2-cyclin E complexes function during meiotic and early emb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: A56186
A;Status: preliminary
A;Status: preliminary
A;Rolcoule type: mRNA
A;Rossius: 1-408 «REM>
A;Coust.
A;Cross-references: UNIPROT:091780; GB:L23857; NID:g431745; PIDN:AAA73524.1; PID:g43174
B;Couturier, A.; Philippe, M.
B;Couturier to the EMBL Data Library, June 1992
A;Description: Cloning and expression of Xenopus cyclin E.
A;Reference number: S34125
A;Status: preliminary
A;Status: preliminary
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C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C.Accession: T00133
protein Rv3618 - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ښ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 36.6%; Score 42.5; DB 2; Length 395; Best Local Similarity 30.0%; Pred. No. 51; Matches 6; Conservative 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 408;
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A;Residues: 1-32,'A',34-199,'NV',202-258,'GN',261-408
A;Cross-references: EMBL:Z13966
C;Superfamly: cotolin, ABDD/E type
C;Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 SWFNVFLQVAYIRELQQFLRPQFPQE 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:::|: : |||:
157 WFTLREAOLHIRPYTWPYPE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 WYSMRKMSMKIRPF---FPQ 20
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C; pate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change.
C; pate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change.
C; pate: 05-Dec-1997 #sequence, V.; Carter, N.M.; Change.
C; pate: 05-Dec-1997 #sequence, V.; Carter, N.M.; Change.
C; pate: 05-Dec-1997 #sequence, V.; Fuma, S.; Galizzi, A.; Galler
A; Aluthors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
Scotter, P.; Kondingstein, G.; Krogh, S.; Kumano, M.; Kuita, K.; Lapdue, S.; Muello, M.;
A; Muthors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Kuita, K.; Lapdue, S.; Muello, S.; Muello, S.; Muchors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekjauch, J.; Sakowska, A.; Sarlo, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekjauchi, J.; Sekowska, A.; Sekouchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Vasumoto, V.; Voshida, R.; A; Title: The complete genome sequence of the Gram-postive bacterium Bacillus subtilis.
A; Rieference number: A69580; MUID:98044033; PMID:9384377
A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Redecule type: DNA
                                                                                                                                                                   Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Rimatchews, L.
submitted to the EMBL Data Library, September 1999
A;Reference number: 220365
A;Accession: T27431
A;Accession: T27431
A;Accession: T27431
A;Residues: preliminary; translated from GB/EMBL/DBJ
A;Residues: 1-2129 < WIL>
A;Residues: 1-2129 < WIL>
A;Cross-references: UNIPROT:Q9UIR8; EMBL:AL110501; NID:e1542357; PIDN:CAB54509.1; CESP:Y
Cisperimental source: clone Y79H2A
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: CBSP:Y79H2A.3
A;Introne: 39/3; 75/1; 125/3; 212/3; 254/1; 330/3; 460/1; 486/3; 540/3; 580/3; 631/1;
; 1760/1; 1929/3; 2037/3; 2074/3
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                                                                                                                                                 Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Accession: T27431
Matthews, L.
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43.8%; Pred. No. 2.3e+02;
tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 75;
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                                                                                                                                   - Caenorhabditis elegans
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Pred. No. 9.5;
6; Mismatches 5;
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Best Local Similarity 36.8%;
Matches 7; Conservative (
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RESULT 32 C70957

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A;Cross-references: UNIPROT:Q9US42; EMBL:D89119; NID:g1749445; PIDN:BAA13781.1; PID:g17
A;Experimental source: strain PR745
C;Superfamily: Schizosaccharomyces hypothetical 44.2K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F28N24.15 - Arabidopsis thaliana ($\text{Cispecies}$; Arabidopsis thaliana ($\text{mouse-ear}$ cress$)

C;Bate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Bate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Bate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86414
C;Accession: A86414
C;Bate: 02-Mar-2001 M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: A$6414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPROT: Q9LP45; GB: AE005172; NID: 99502423; PIDN: AAF88122.1; GSPDB: G
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C;Superfamily: Caenorhabditis elegans 268 proteasome regulatory complex chain p44.5
                                                                                                                                                                                                                                                                                                     Cispecies: Schizosaccharomyees pombe
Cispecies: Schizosaccharomyees pombe
Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
Cibacession: T42242
A; Status: plantification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: 217323; MUID:98162722; PMID:9501991
A;Accession: T42242
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-399 <YOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19S proteosome subunit 9 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #sequence_revision 20-Oct-2000 #sejun: TS2033
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                                                                                                                                                                                                                                                                                    hypothetical 44.2% protein - fission yeast (Schizosaccharomyces pombe)
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Pred. No. 65;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.2%; Score 42; DB
53.3%; Pred. No. 62;
iive 3; Mismatches
                                                     SYVDLDKIPKSLRPFFP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 GSWKSGRIIAKKLRP 383
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        SWYSMRKMSMKIRPFFP
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Matches 7; Conservative
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LRKLLTKLRPFF 74
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Best Local Similarity
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                                                                                                                                                A.Accession: T00133
A.Status: translated from GB/EMBL/DDBJ
A.Status: translated from GB/EMBL/DDBJ
A.Residues: 1-2925 enonic RNA
A.Residues: 1-2925 enonic RNA
A.Residues: U-2925 enonic RNA
A.Residues: 1-2925 enonic RNA
A.Residues: 1-2925 enonic RNA
A.Residues: 1-2925 enonic RNA
A.Residues: 1-2925 enonic RNA
A.Residues: nucleotidyltransferase
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C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: D71514
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Itle: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track, A;Accession: D71514
A;Status: preliminary
A;Accession: D71514
A;Status: D71514
A;Brainiary
A;Reiniary
A;Reiniary
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Cipate: 30.Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
Cipate: 30.Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
Cipate: 30.Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
Cipate: Cipat
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A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: cysJ
                                                                                      gend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable sigma 54 modulation protein [imported] - Agrobacterium tumefaciens (strain C58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-210 «KUR»
A;Cross-references: UNIPROT:Q8UIG6; GB:AE007869; PIDN:AAK86148.1; PID:g15155237; GSPDB:
R;Toriyama, S.; Kimishima, T.; Takahashi, M.; Shimizu, T.; Minaka, N.; Akutsu, K. J. Gan. Vitzol. 79, 2051-2058, 1998
A;Title: The complete nucleotide sequence of the rice grassy stunt virus genome and A;Reference number: Z14118; WUID:98178059; PMID:9714257
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C;Species: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42.5; DB 2;
Pred. No. 3.9e+02;
4; Mismatches 6;
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36.2%; Score 42; DB

Best Local Similarity 41.2%; Pred. No. 54;

Matches 7; Conservative 4; Mismatches
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Best Local Similarity 52.99
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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A;Gene: AGR_C_579
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conjugal transfer protein trbE [imported] - Agrobacterium tumefaciens (strain C58, Dupo C,Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein U60-U66 - human herpesvirus 7 (strain JI)
C;Species: human herpesvirus 7
A;Variety: strain JI
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41963
K;Nicholas, J.
Submitted to the EMBL Data Library, December 1995
A;Description: Determination and analysis of the complete nucleotide sequence of human A;Reference number: Z22022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F9N11.50 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Cipate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 (Cipate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 (Cipate: 20-Sep-1999 #sequence_revision Pr; Smith, A.; Bancroft, I.; Mewes, H.W.; Mayer, Reference number: 217873 A; Reference number: 217873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-663 <NIC>
A;Cross-references: UNIPROT:P52462; EMBL:U43400; PIDN:AAC54723.1
                                               Length 607
                                                                                                               6; Indels
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A,Cross-references: UNIPROT:09SUM4; EMBL:AL109796
A,Experimental source: cultivar Columbia; BAC clone F9N11
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Pred. No. 1.1e+02;
3; Mismatches 3;
                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: T41963
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                               36.2%; Score 42; DB
36.8%; Pred. No. 95;
tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Note: U60-U66
C, Superfamily: herpesvirus 38K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 SHFVMKDVEFKCRRFFPQK 259
                                                                                                                                                                        2 GSWYSMRKMSMKIRPFFPQ 20
                                                                                                                                                                                                                    38 GIYFLLKEMDPKIDPFSPE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SWYSMRKMSMKIRPFFPQQ 21
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648 TWYSLRATSQEIR 660
                                           Query Match
Best Local Similarity 36.8
Matches 7; Conservative
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A;Introns: 7/1; 139/1; 349/1
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Best Local Similarity
Matches 8; Conserva
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Best Local Similarity
Matches 7; Conserva
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                                                                                                                                                                                                                                     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Residues: 1-432 - STR.
Cross-references: UNIPROT: P04115, GB: K03049; NID: g213193; PIDN: AAA49262.1; PID: g213194
C, Superfamily: fibrinogen gamma chain; fibrinogen bete/gamma homology
C, Keywords: blood coagulation; glycoprotein; liver; plasma; pyroglutamic acid
C, Keywords: blood coagulation; glycoprotein; liver; plasma; pyroglutamic acid
F; 25-432/Product: fibrinogen gamma chain #status experimental - MPT-
F; 25-Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F; 25/Modified site: carbohydrate (Asn) (covalent) #status predicted
F; 421/Cross-link: isopeptide (Gln) (interchain to Lys-425 N6-amino) #status predicted
F; 425/Cross-link: isopeptide (Lys) (interchain to Gln-421) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Petromyzon marinus (sea lamprey)
C; Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C; Jozession. 403129
R; Strong, D.D.; Moore, M.; Cottrell, B.A.; Bohonus, V.L.; Pontes, M.; Evans, B.; Riley, Biochemistry 24, 92-101, 1985
A; Title: Lamprey fibrinogen gamma chain: cloning, cDNA sequencing, and general character A; Reference number: A03129; MUID:85199776; PMID:2581603
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R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Offuku, Y.; Punahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug_1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
RiStaub, J.M.; Kwok, S.F.; Deng, X.W.
submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana homologue of human 198 proteosome subunit S9.
A;Reference number: 225911
A;Reference number: 225911
A;Reference number: 225913
A;Reference: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: manolocule type: manolocule type: manolocule type: manolocule type: manolocule type: manolocule type: A;References: UNIPROT:081694; EMBL:AF083890; PIDN:AAC34120.1
C;Superfamily: Caenorhabditis elegans 26S proteasome regulatory complex chain p44.5
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C;Species: Petromyzon marinus (sea lamprey)
C;Date: 17-Mar_1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
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Pred. No. 65;
3; Mismatches 2; Indels
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Pred. No. 67;
4; Mismatches 3; Indels
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398 WYSLKMTTMKLLP 410
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Best Local Similarity 58.3
Matches 7; Conservative
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LRKLLTKLRPFF 74
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Best Local Similarity
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A, Status: preliminar
A, Molecule type: DNP
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Gaps

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A;Molecule type: DNA
A;Residues: 1-1025 <STO>
A;Cross-references: UNIPROT:Q9HXW4; GB:AE004787; GB:AE004091; NID:g9949835; PIDN:AAG070:
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-1648 <ROS>
A;Cross-references: UNIPROT:P47171; EMBL:Z49640; NID:g1015881; PID:g1015882; MIPS:YJR14
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A;Cross-references: UNIPROT:Q06554; EMBL:U20865; NID:g662330; PID:g662344; GSPDB:GN0001
A;Cross-references: UNIPROT:Q06554; EMBL:U20865; NID:g662330; PID:g662344; GSPDB:GN0001
C;Gentimental source: strain S288C (AB972)
C;Gene: MIPS:YLR247c
A;Gene: MIPS:YLR247c
A;Cross-references: SGD:S0004237
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NyAlternate names: hypothetical protein J2161
C;Species: Saccharomyces cerevisiae
C;Species: O8-dul-1995 #sequence_revision O8-Sep-1995 #text_change O9-Jul-2004
C;Accession: S57163; S57169
C;Accession: S57163; S57169
R;Rose, M.; Koetter, P.; Entian, K.D.
Submitted to the Protein Sequence Database, September 1995
A;Reference number: S56848
A;Accession: S57163
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NiAlternate names: hypotherical protein 19672.14
C.Species: Saccharomyces cerevisiae
C.Species: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
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C;Superfamily: Saccharomyces cerevisiae probable membrane protein YJR140c
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                                                                                                                                                                                                                    Length 1025;
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submitted to the Protein Sequence Database, September 1995
A;Reference number: 857169
A;Accession: 857169
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                                                                                                                                                                                                                    Score 42; DB 2;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                     1; Mismatches
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A,Residues: 1-1647 <SCA>
A,Cross-references: EMBL:Z49640; MIPS:YJR140c
C,Genetics:
C,Gene: SOD:HIR3
A,Cross-references: SGD:S0003901; MIPS:YJR140c
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                                                                                                                                                                                                                  Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
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                   C; Accession: AD3232
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I serage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-1015 <STO>
A;Cross-references: UNIPROT:Q916X4; GB:AE004453; GB:AE004091; NID:g9945978; PIDN:AAG0354
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-822 «KUR»
A;Cross-references: UNIPROT:Q9R488; GB:AE008690; PIDN:AAL46274.1; PID:g17744055; GSPDB:
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                           ster, E.W.
Ayîtile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD3232
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Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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Pred. No. 1.3e+02;
2; Mismatches 4; Indels
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Matches 8; Conservative
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C, Superfamily: virB4 protein
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Gaps

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Length 210 8; Indels

Score 41; DB 2; Pred. No. 47; 6; Mismatches

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F;96-112/Domain: transmembrane #status predicted <TM3>
F;141-157/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                              Search completed: January 18, 2005, 11:04:48 Job time : 42 secs
                                                                                                                                                                                                                                        156 GLWYSNWDLQKRLKEFYAQE 175
                                                                                                                                                                                                       2 GSWYSMRKMSMKIRPFFPQQ 21
                                                                                       35.3%;
                                                                                                                                             Conservative
                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
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A; Readdues: 1-210 <8CH5
A; Cross-references: UNIPROT:Q12413; EMBL:Z74260; NID:g1431353; PIDN:CAA98790.1; PID:e253
A; Experimental source: strain $288C
B; Ljungdahl, P.O.; Gimeno, C.J.; Styles, C.A.; Fink, G.R.
Cell 71, 463-478, 1992
A; Title: SRR3: a novel component of the secretory pathway specifically required for loca
A; Reference number: $31270; MUID:93046646; PMID:1423607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: B90464
A; Status: preliminary
A; Molecule type: DNA
A; Regidueg: 1-147 < KUR>
A; Cross-references: UNIPROT: Q97UX9; GB: AE006641; NID: g13816220; PIDN: AAK42969.1; GSPDB: G
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: B99464
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, T.; Jefffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
                                                                                                                                                                                                          ;
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NyAlternate names: protein D1022; protein YDL212w
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67771; S312.70
R;Schmidt, E.R.; Bahr, A.; Kraemer, C.; Hankeln, T.; Moeller-Rieker, S.
Bubmitted to the Protein Sequence Database, July 1996
A;Reference number: S67756
                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May_2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reaidues: 1-124,'EKLR', 130-210 <LJU>
A;Cross-references: EMBL:L01264; NID:g172571; PIDN:AAA35035.1; PID:g172572
                                                                                                                                                                                                       Gaps
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                                                                                                                                    Score 41.5; DB 2; Length 1556;
Pred. No. 3e+02;
3; Mismatches 3; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                        C;Refwords: transmembrane protein
P;1235-1282/Domain: RING finger homology <RRN>
F;1236-1252/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 4L
C;Keywords: endoplasmic reticulum; transmembrane protein
F;10-26/Domain: transmembrane #status predicted <TML>
F;62-78/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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41.2%; Pred. No. 33;
tive 6; Mismatches
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130 GTWYIIRDKKINMNVQP 146
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268 YSKDRLS-KIKPFLPQ 282
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                                                                                                                                                                                                                                                          5 YSMRKMSMKIRPFFPO 20
                                                                                                                                       Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
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Best Local Similarity 41.2<sup>3</sup>
Matches 7; Conservative
   A; Map position: 12R
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January 18, 2005, 11:08:15; Search time 146 Seconds (without alignments) 51.966 Million cell updates/sec
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(cgnz_6/ptodata1/pubpaa/USO7_NEW_PUB.pep:*
(cgnz_6/ptodata1/pubpaa/USO6_PUBCOMB.pep:*
(cgnz_6/ptodata1/pubpaa/USO6_PUBCOMB.pep:*
(cgnz_6/ptodata1/pubpaa/USO6_PUBCOMB.pep:*
(cgnz_6/ptodata1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1608061 seqs, 361289386 residues
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Maximum Match 100%
Listing first 65 summaries
                                                                                                                                                              OM protein - protein search, using sw model
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1 KGSWYSMRKMSMKIRPFFPQQ 21
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 185, App	Sequence 6, Appli	Sequence 33, Appl	Sequence 11, Appl	Sequence 1, Appli	Sequence 27, Appl	Sequence 171, App	Sequence 66, Appl	Sequence 41, Appl	Sequence 41, Appl	Sequence 114, App	Sequence 102, App	Sequence 7, Appli
	ID	US-09-989-920-185	US-10-017-724-6	US-09-919-039-33	US-10-181-187D-11	US-10-181-187D-1	US-10-298-461-27	US-10-648-593-171	US-10-733-969A-66	US-10-372-735-41	US-10-608-541-41	US-10-372-735-114	US-10-608-541-102	US-10-181-187D-7
	DB	6	14	10	16	16	14	16	17	14		14		
	Query Match Length DB	489	491	488	16	20	242	437	453	20	20	27	27	10
æ	Query	100.0	100.0	97.4	51.7	51.7	51.7	51.7	51.7	50.0	50.0	50.0	50.0	49.1
	Score	116	116	113	9	9	9	9	9	58	58	58	28	57
	Result No.	-1	8	m	4	2	9	7	œ	6	10	11	12	13

e 1, 7	Sequence 28	Se 28	equence 28,	equence 28	ednence 28	equence 28	Sequence 23	e 3,	equence 2,	'n	equence 62.	а 2 - 2	quence 689	equence 46	eguence 26	98	equence 6,	equence 10	equence 3,	24	equence 21	equence 46	e 48	equence 4,	equence 4,	Seguence 4, Appli	equence 4,	equence 4,	4,	equence 6,	Sequence 4, Appli	equence 4.	equence 4,	Sequence 8,	ence 4,	equence 14,	rence	лсе 6,	equence 6,	equence 7,	equence 8,	, o	'e anianha
-912-741B-1 -912-740A-1	US-09-992-600A-28	-09-924-340-2	US-09-999-570-28	US-10-000-489-2	US-10-000-986-2	US-10-154-678-28	US-09-832-355A-	US-10-112-527-3	US-10-112-527-	-10-112-527-1	US-10-262-122A-6213	US-10-112-527-4	US-09-738-626-6	US-10-494-674-46	US-10-424-599-2	US-10-114-270-8	US-10-181-187D-	US-10-298-461-1	-07-181-01-00 -130-00-01-31	-10-236-461- -09-832-355A	US-09-832-355A-2	US-10-351-161A-	US-10-351-161A	US-10-223-085-	8-10-223-08	US-10-223-088-	US-10-223-087-	S-10-223-083-	US-10-223-089-	S-10-394-557-	115-10-223	US-10-305-654-	S-10-081-056-	US-10-225-060	09-998-831-4	US-09-897-306-1	S-09-998-833-	US-10-179-744	US-10-186-817-	US-10-215-224-	US-10-215-224	- C10 - V1C	-218-417-01-60
411 9	82 1	20	82 1	82 1	82 1	787	17 1	21 1	36 1	51 .	1.	47 1	643 9	646 1	844 1	017 1		•	17	1 6	21 1	79 1	42 1	70	0 0	202	70	70	70		9 6	70	70 1	80 1	9	96	96 1	96	96	96	9 4	96	9
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14	17	18	50	21	22	23	25	56	27	58	62	31	32	33	34	32	9 19	7 0 0	0 0	y 4.	41	42	43	44	2 4 5	. 74	48	4	20	51	20 6	40	55	99	57	28	29	09	61	62		# u	

ALIGNMENTS

US-09-989-920-185

Sequence 185, Application US/0998920

Patent No. US20020172957A1

GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen,

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OTHER INFORMATION: Equivalent to the c-terminus of fibrogen gamma-chain
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.7%; Score 60; DB 16; Length 20; 64.7%; Pred. No. 0.1;
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(16); OTHER INFORMATION: Xaa is any amino acid or is absent US-10-181-187D-11
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Haptotactic consensus sequence
                                                                                                                                                                           US-10-181-187D-11
| Sequence 11, Application US/10181187D | Publication No. US20040126758A1 |
| GENERAL INPORMATION: | APPLICANT: GERAED WARX |
| APPLICANT: RAPHAEL GORODETSKY |
| TITLE OF INVENTION: NOVEL HAPTOTACTIC PEPTIDES |
| FILE REFREENCE: 10/181,187 |
| CURRENT APPLICATION NUMBER: US/10/181,187D |
| CURRENT FILING DATE: 2003-10-20 |
| PRIOR APPLICATION NUMBER: US/9/487790 |
| NUMBER OF SEQ ID NOS: 12 |
| SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10181187D

Publication No. US20040126758A1

GENERAL INFORMATION:
APPLICANT: GEARD MARX

TITLE OF INVENTION: NOVEL HAPTOTACTIC PEPTIDES

FILE REFERENCE: 10/181,187D

CURRENT APPLICATION NUMBER: US/10/181,187D

CURRENT FILING DATE: 2003-10-20

PRIOR APPLICATION NUMBER: US/9/487790

PRIOR PILING DATE: 2000-01-20

NUMBER OF SEQ ID NOS: 12

SOSTWARE: PATENTIN VERSION 3.1
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                           468 KGSWYSMKKMSMKIRPFFPQQ 488
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                                               1 KGSWYSMRKMSMKIRPFFPQQ
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1 KTRWYSMKKTTMKIIPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KGSWYSMRKMSMKIRP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KGXXYSMRKXXMKIRP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial sequence
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  20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC_FEATURE
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LENGTH: 20
TYPE: PRT
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LENGTH: 16
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Sequence 33, Application US/09919039

Sequence 33, Application US/09919039

Sequence 33, Application US/09919039

Publication No. US20030108871A1

GENERAL INFORMATION:

APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES

CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOSTWARE: PERL PROGRAM
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                                                                                                                                                                                                                                 Gaps
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; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MAI-004
; FILE REFERENCE: MAI-004
; CURRENT APPLICATION NUMBER: US/10/017,724
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR PILING DATE: 2001-10-05
; PRIOR PILING DATE: 2001-10-16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-017-724-6
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NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. US20030108871A1 3393861CD1
US-09-919-039-33
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Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 21; Conservative 0; Mismatches 0;
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Pred. No. 3.3e-08;
                                                                                                                                                                                                                                                                                                     469 KGSWYSMRKWSMKIRPFFPQQ 489
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                                                                                                                                                                                                                                                                         1 KGSWYSMRKMSMKIRPFFPQQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10017724
Publication No. US20030099958A1
GENERAL INFORMATION:
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95.2%;
                     SOFTWARE: Patentin version 3.1
SEQ ID NO 185
  NUMBER OF SEQ ID NOS: 284
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                                                                                                            ; ORGANISM: Homo sapien
US-09-989-920-185
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Best Local Similarity
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LENGTH: 488
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                                                                                      TYPE: PRT
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NUMBER OF SEQ ID NOS: 199
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Fibrinogen gamma chain precursor; OTHER INFORMATION: Accession NO: as of 29 August 2003: P02679
APPLICANT: LIU, TONG HUA
APPLICANT: LU, ZHAO HUI
APPLICANT: LU ZHAO HUI
APPLICANT: LU ZHAO HUI
TITLE OF INVENTION: SPECIFIC MARKERS FOR PANCRATIC CANCER
FILE REFERENCE: 215.25
CURRENT APPLICATION NUMBER: US/10/733,969A
CURRENT APPLICATION NUMBER: EP 02028058.2
PRIOR APPLICATION NUMBER: EP 02028058.2
NUMBER OF SEQ ID NOS: 110
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn version 3.2
SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 51.7%; Score 60; DB 17; Length 453; 1 Similarity 64.7%; Pred. No. 1.7; 11; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: USZUGISZSZSIAI

APPLICATION NO. USZUGISZSZSIAI

APPLICANT: Sallberg, Matti
TITLE OF INVENTION: SAPECIFICITY EXCHANGERS THAT REDIRECT
TITLE OF INVENTION: ANTIBODIES TO A PATHOGEN
FILE REFERENCE: TRIPEP.7AUC4CP1
CURRENT APPLICATION NUMBER: US/10/372,735
CURRENT APPLICATION NUMBER: US/202-02
PRIOR PELING DATE: 2001-04-19
PRIOR PELING DATE: 2001-04-19
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 1095-02-08
PRIOR PELING DATE: 1995-12-27
PRIOR APPLICATION NUMBER: US/32,085
PRIOR PELING DATE: 1995-12-27
PRIOR APPLICATION NUMBER: US/64,945
PRIOR APPLICATION NUMBER: US/64,945
PRIOR PELING DATE: 1995-00-09-19
PRIOR PELING DATE: 1995-00-09-19
PRIOR PELING DATE: 2000-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-372-735-41
; Sequence 41, Application US/10372735
; Publication No. US20030225251A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 KTRWYSMKKTTMKIIPF 415
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 11; Conserva
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Sequence 171, Application US/10648593
Publication No. US20040106132A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILE REPERENCE: D0273 NP
CURRENT APPLICATION NUMBER: US/10/648,593
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: 60/406,385
PRIOR FILING DATE: 2002-08-27
                                                                                                                                                                                                  APPLICANT: Genber, Hans-Peter
APPLICANT: Kowalski, Joe
APPLICANT: Kowalski, Joe
APPLICANT: Fisabarro, Maria Teresa
APPLICANT: Fisabarro, Maria Teresa
APPLICANT: Fisabarro, Maria Teresa
APPLICANT: Sherman, Daniel Eric
TITLE OF INVENTION: COMPOSITION COMPRISING AND METHOD OF
TITLE OF INVENTION: USING ANGIOGENIC FACTOR ANGIOPOIETIN-LIKE PROTEIN 3 ANGPTL3
FILE REPERENCE: GENENT: 086A
CURRENT FILING DATE: 2002-11-15
PRIOR PILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FestSEQ for Windows Version 4.0
SEQ ID NO 27
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; Sequence 66, Application US/10733969A
; Publication No. US20040219572A1
; GENERAL INFORMATION:
APPLICANT: CHEN, JIE
                                                                                              Sequence 27, Application US/10298461
Publication No. US20030215451A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 171
LENGTH: 437
                                                                                                                                                                                APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hans-Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 64.74
Matches 11; Conservative
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CORGANISM: Homo sapiens
US-10-298-461-27
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US-10-648-593-171
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Best Local Similarity
Matches 11; Conserv
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GENERAL INFORMATION:

JEDUICANT: Matti Sallberg

TITLE OF INVERNION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS

TITLE OF INVERNION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS

TITLE OF INVERNION: THAT REDIRECT ANTIBODIES TO RECEPTORS ON A PATHOGEN

FILE REPERENCE: TRIPEP.007CP3C1

CURRENT APPLICATION NUMBER: U5/664,945

PRIOR PELING DATE: 2003-06-27

PRIOR PELING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 09/532,106

PRIOR APPLICATION NUMBER: 09/246,258

PRIOR APPLICATION NUMBER: 09/246,258

PRIOR PELING DATE: 1990-02-08

PRIOR FILING DATE: 1995-04-27

PRIOR FILING DATE: 1995-04-27

PRIOR FILING DATE: 1994-04-28

NUMBER: PABLICATION NUMBER: SE 9401460

PRIOR FILING DATE: 1994-04-28

NUMBER: PABLICATION NUMBER: SE 9401460

PRIOR FILING DATE: 1996-12-7

PRIOR FILING DATE: 1996-12-7

PRIOR FILING DATE: 1996-12-7

PRIOR FILING DATE: 1996-12-7

PRIOR FILING DATE: 1996-10-27

PRIOR FILING DATE: 1996-10-27
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PRIOR APPLICATION NUMBER: 09/664,945
PRIOR FILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2001-09-19
PRIOR PLING DATE: 2001-09-19
PRIOR PLING DATE: 2001-09-19
PRIOR PILING DATE: 2002-05-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEC ID NOS: 199
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-608-541-102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 50.0%; Score 58; DB Best Local Similarity 71.4%; Pred. No. 0.26 Matches 10; Conservative 2; Mismatches
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; Sequence 102, Application US/10608541
; Publication No. US20040019189A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 71.4%;
Matches 10; Conservative
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WYSMKKTTMKIIPF 15
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US-10-181-187D-7
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GENERAL INFUGATION:
GENERAL INFUGATION:
JIGAND/RECEPTOR SPECIFICITY EXCHANGERS
TITLE OF INVENTION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS
TITLE OF INVENTION: LIGAND/RECEPTOR ANTIBODIES TO RECEPTORS ON A PATHOGEN
FILE REFERENCE: TRIPEP. 007CP3C1
CURRENT APPLICATION NUMBER: US/10/608,541
CURRENT PELLICA DATE: 2003-06-27
PRIOR PELLICATION NUMBER: 09/664,945
PRIOR FILING DATE: 2000-03-21
PRIOR PELLICATION NUMBER: 09/246,258
PRIOR FILING DATE: 1999-02-08
PRIOR PELLICATION NUMBER: PCT/SE 95/00468
PRIOR PELLING DATE: 1996-12-27
PRIOR PELLING DATE: 1996-12-27
PRIOR PELLING DATE: 1996-04-27
PRIOR FILING DATE: 1996-04-28
PRIOR FILING DATE: 1996-04-28
PRIOR FILING DATE: 1994-04-28
NUMBER OF SEQ ID NOS: 105
SEQ ID NO 41
LENGTH: 20
TENGRAPH: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT SAILDERG, MALLI

TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
TITLE OF INVENTION: ANTIBOLES TO A PATHOGEN
FILE REFERENCE: TRIPEP. 7AUG4CP1
CURRENT FILING DATE: 2003-02-21
PRIOR PELING DATE: 2002-08-30
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: 09/83, 666
PRIOR APPLICATION NUMBER: 09/83, 106
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-02-08
                                                   Indels
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    71.4%; Pred. No. 0.2;
tive 2; Mismatches
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APPLICATION NUMBER: PCT/SE95/00468
FILING DATE: 1995-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 114, Application US/10372735
Publication No. US20030225251A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 41, Application US/10608541 Publication No. US20040019189A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                            4 WYSMRKMSMKIRPF 17
                                                                                                                                                                               2 WYSMKKTTMKIIPF 15
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                                               10; Conservative
        Best Local Similarity
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                                                   Matches
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Sequence 1. Application US/09912740A

| Sequence 1. Application US/09912740A
| Patent No. US20020169280A1
| GENERAL INFORMATION:
| APPLICANT: Altiari, Dario C
| APPLICANT: Altiari, Dario C
| APPLICANT: Thornton, George B
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
| FILE REPRENCE: 300.1Div3
| CURRENT FILING DATE: 1999-07-06
| PRIOR FILING DATE: 1999-07-06
| PRIOR FILING DATE: 1996-11-12
| PRIOR FILING DATE: 1996-11-12
| PRIOR FILING DATE: 1994-04-25
| PRIOR FILING DATE: 1993-10-19
| PRIOR FILING DATE: 1993-10-19
| PRIOR FILING DATE: 1993-10-19
| PRIOR FILING DATE: 1993-06-12
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                              DB 9; Length 411;
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                                                                                     5; Indels
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49.1%; Score 57; DB 5
Best Local Similarity 64.7%; Pred. No. 4.3;
Matches 11; Conservative 1; Mismatches
                        49.1%; Score 57; DB 64.7%; Pred. No. 4.3; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: site of glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 46553, Application US/09864761
Patent No. US20020048763A1
GENERAL INPORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: DISULFID
CCATION: (326)...(339)
OTHER INFORMATION: disulfide-bond
US-09-912-740A-1
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NAME/KEY: DISULFID
LOCATION: (153)...(182)
OTHER INFORMATION: disulfide-bond
                                                                                                                                                                                373 KTRWYSMKKTIMKIIPF 389
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                                                                                                                                           1 KGSWYSMRKMSMKIRPF 17
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Query Match
Best Local Similarity 64...
Best Local Similarity 64...
The 11; Conservative
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LOCATION: 88
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ORGANISM: Unknown
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US-09-912-740A-1
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Patent No. US20020131970A1
GENERAL INFORMATION:
APPLICANT: Languino, Lucia R
APPLICANT: Languino, Lucia R
TITLE OF INVENITON: METHODS AND COMPOSITIONS FOR INHIBITING
TITLE OF INVENITON: METHODS AND COMPOSITIONS FOR INHIBITING
TITLE OF INVENITON: METHODS AND COMPOSITIONS FOR INHIBITING
TITLE OF INVENITON: MENDOTHELLAL CELL AND FIBRINOGEN MEDIATED INFLAMMATION
FILE REFERENCE: 300.1Div4
CURRENT APPLICATION NUMBER: US/09/912,741B
CURRENT APPLICATION NUMBER: US 09/347,877
PRIOR FILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-06
PRIOR PELING DATE: 1994-04-25
PRIOR APPLICATION NUMBER: US 08/139,562
PRIOR FILING DATE: 1993-10-19
PRIOR FILING DATE: 1993-10-19
PRIOR FILING DATE: 1993-04-15
PRIOR FILING DATE: 1993-04-15
PRIOR FILING DATE: 1993-04-15
PRIOR FILING DATE: 1993-06-12
PRIOR FILING DATE: 1992-06-12
PRIOR FILING DATE: 1992-06-12
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49.1%; Score 57; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels
                  GENERAL INFORMATION:
APPLICANT: GERARD MARX
TITLE OF INVENTION: NOVEL HAPTOTACTIC PEPTIDES
FILE REFERENCE: 10/181,187
CURRENT FILING DATE: 2003-10-20
PRIOR FILING DATE: 2000-01-20
PRIOR PILING DATE: 2000-01-20
SOFTWARE PERIOR INVEST: 12
SOFTWARE PERIOR IN VERSION 3.1
SEQ ID NO 7
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OTHER INFORMATION: site of glycosylation
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CCATION: (326)...(339)

OTHER INFORMATION: disulfide-bond
US-09-912-741B-1
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NAME/KEY: DISULFID
LOCATION: (153)...(182)
OTHER INFORMATION: disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial sequence
Publication No. US20040126758A1
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ORGANISM: Unknown
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LENGTH: 411
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Sequence 28, Application US/09924340

Publication No. US20030027248A1

GENERAL INFORMATION:

APPLICANT: Bejanin, Stephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REPERENCE: 31. US2. REG

CURRENT APPLICATION NUMBER: US/09/924,340

CURRENT APPLICATION NUMBER: US 60/305,456

PRIOR APPLICATION NUMBER: US 60/305,456

PRIOR FILING DATE: 2001-07-13

PRIOR PLILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/298,698

PRIOR APPLICATION NUMBER: US 60/298,698

PRIOR PLILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 112
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Pred. No. 4.3;
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                              TILE KTE FERELS 31.09.101.

CURRENT FILING DATE: 2001-11.13

PRIOR APPLICATION NUMBER: US/09/922,600A

PRIOR FILING DATE: 2001-11.13

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-08-06

PRIOR PLING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: PCT/IB01/01715

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-06-19

PRIOR FILING DATE: 2001-06-19

PRIOR FILING DATE: 2001-06-19

PRIOR FILING DATE: 2001-06-15

PRIOR PILING DATE: 2001-06-15

PRIOR 280 ID NOS: 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Xaa = Phe, Ser US-09-992-600A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 233
; OTHER INFORMATION: Xaa = Phe, Ser
US-09-924-340-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.3%;
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OTHER INFORMATION: Xaa
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NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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US-09-924-340-28
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LENGTH: 282
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      INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ï
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INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 14
INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 18
INFORMATION: SWISSPROT HIT: PL2799, EVALUE 1.00e-09
INFORMATION: EST_HUMAN HIT: AA677287.1, EVALUE 5.00e-27
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APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9; Length 50;
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SIN TITLE OF INVENTION: HUMAN GENOME-DERIVED SIN TITLE OF INVENTION: GENE EXPRESSION ANALYSI; CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT APPLICATION NUMBER: US/01/80,312 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: US/09/622,366 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: US/09/632,366 PRIOR APPLICATION NUMBER: US/09/632,366 PRIOR FILING DATE: 2000-09-37 PRIOR PRILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: US/09/63,359 PRIOR FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00669 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00663 PRIOR FILING DATE: 2001-01-30 PRIOR FILING DATE: 2000-09-21 PRIOR PRIOR FILING DATE: 2000-09-21 PRIOR PRIOR FILING DATE: 2000-09-21 PRIOR FILING DATE: 2000-09-21 PRIOR PRIOR FILING DATE: 20
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Best Local Similarity 55.0°
Matches 11; Conservative
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260 GWWYSLKSVVMKIRPNDFIP 279
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; OTHER INFORMATION: Xaa = Phe, Ser
US-09-999-570-28
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OTHER INFORMATION: Xaa = Asn, Thr
NAME/KEY: UNSURE
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55.0%;
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Best Local Similarity 55.0%;
Matches 11; Conservative
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; Sequence 28, Application US/100
; Publication No. US20030092011A1
                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 116
OTHER INFORMATION: Xaa
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Best Local Similarity
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                                                    Gaps
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APPLICANT: Tanaka, Hiroaki
ITLEOF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.USS.DIV
CURRENT APPLICATION HUMBER: US/09/992,095B
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PLING DATE: 2001-08-06
PRIOR PLING DATE: 2001-08-06
PRIOR PLING DATE: 2001-07-13
PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/298,69B
PRIOR PELING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 112
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Publication No. US20030170628A1
| GENERAL INFORMATION:
| APPLICANT: Benjain, Stephane
| APPLICANT: Tanaka, Hiroaki
| TITLE OF INVENTION: HUMAN CONAS AND PROTEINS AND USES THEREOF
| FILE REFERENCE: G-091US08DIV
| CURRENT FILING DATE: 2001-06-14
| PRIOR FILING DATE: 2001-08-06
     DB 10; Length 282;
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ch 48.3%; Score 56; DB Similarity 55.0%; Pred. No. 4.3; 11; Conservative 3; Mismatches
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Best Local Similarity 55.0%; Pred. No..
Matches 11; Conservative 3; Mismatr
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; Sequence 28, Application US/09992095B
; Publication No. US20030157485A1
; GENERAL INFORMATION:
                                                                                                                                  260 GWWYSLKSVVMKIRPNDFIP 279
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                                                                                                  2 GSWYSMRKMSMKIRP--FFP 19
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US-09-992-095B-28
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ORGANISM: Homo sapiens
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Query Match
Best Local Similarity
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| APPLICANT: Benjanin, Stephane
| APPLICANT: Tanaka, Hiroaki
| TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
| FILE REFERENCE: 91.USG. DIV
| CURRENT FILING DATE: 2001-11-14
| PRIOR PRILOGATION NUMBER: US/924,340
| PRIOR APPLICATION NUMBER: US 09/924,340
| PRIOR PLILNG DATE: 2001-08-06
| PRIOR PLILNG DATE: 2001-08-06
| PRIOR FILING DATE: 2001-08-06
| PRIOR PLILNG DATE: 2001-06-05
| PRIOR PLILNG DATE: 2001-06-05
| PRIOR PLING DATE: 2001-06-29
| PRIOR PLING DATE: 2001-06-29
| PRIOR PLING DATE: 2001-06-25
| PRIOR PLING DATE: 2001-06-15
| SOFTWARE: JBatent
| SEC ID NO 28
| LENGTH: 202
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3; Mismatches
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Pred. No. 4.3;
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR PILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 28
LENGTH: 282
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-1082
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Patent No. US2002052308A1

GENERAL INFORMATION:

APPLICANT: ROSen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2000-03-08

PRIOR PILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: PATENTIN VOY: 2.0
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Pred. No. 5.1;
3; Mismatches 4; Indels
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APPLICANT: Kessler, Paul
TITLE OF INVENTION: VEGF FUSION PROTEINS
FILE REFERENCE: 205654
CURRENT APPLICATION NUMBER: US/09/832,355A
CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 28
LENGTH: 282
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, Sequence 23, Application US/09832355A
; Publication No. US20030027751A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                            LOCATION: 116
OTHER INFORMATION: Xaa = Asn,Thr
                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 233
; OTHER INFORMATION: Xaa = Phe, Ser
US-10-154-678-28
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Best Local Similarity 55.0%;
Matches 11; Conservative
                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
....hes 11; Conserve
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NAME/KEY: UNSURE
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LENGTH: 339
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US-10-000-986-28
Squence 28, Application US/10000986
Squence 28, Application US/10000986
Publication No. US20030096247A1
GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US9.DIV
CURRENT APPLICATION NUMBER: US 09/924,340
PRIOR PLION DATE: 2001-11-14
PRIOR PLING DATE: 2001-08-06
PRIOR PLING DATE: 2001-08-10
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-25
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APPLICANT: Benjain, Stephane
APPLICANT: Benjain, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 182.181.REG
CURRENT PELLING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 69/924,340
PRIOR PELLING DATE: 2001-06-06
PRIOR PELLING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR PLING DATE: 2001-06-29
PRIOR PELLING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR PELLING DATE: 2001-06-15
PRIOR PELLING DATE: 2001-06-15
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48.3%; Score 56; DB 14; Length 282;
Best Local Similarity 55.0%; Pred. No. 4.3;
Matches 11; Conservative 3; Mismatches 4; Indels
  Indels
     4
3; Mismatches
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                                                                                        260 GWWYSLKSVVMKIRPNDFIP 279
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Publication No. US20030162186A1
GENERAL INFORMATION:
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                                                      2 GSWYSMRKMSMKIRP--FFP 19
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LOCATION: 116
OTHER INFORMATION: Xaa = Asn,Thr
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 233
OTHER INFORMATION: Xaa = Phe, Ser
  11; Conservative
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US-10-154-678-28
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  Matches
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Sequence 1, Application US/10112527

| Sequence 1, Application US/202168722A1
| Publication NO. USS/202168722A1
| GENERAL INFORMATION:
| APPLICANT: Grieninger, Gerd
| APPLICANT: Applegate, Dianne
| APPLICANT: Applegate, Dianne
| APPLICANT: Stoike-Steben, Lara
| TILLE OF INVENTION: NO. US. 2020168722A1e1 Cleaved Fragments of Fibrinogen
| TILLE OF INVENTION: NUMBER: US/10/112,527
| CURRENT APPLICATION NUMBER: US 09/373,157
| PRIOR PILING DATE: 1999-08-12
| WUMBER OF SEQ ID NOS: 7
| SEQ ID NO 1
| SEQ ID NO 1
| LENGTH: 251
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUBBR: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB 13; Length 251;
Pred. No. 21;
4; Mismatches 6; Indels
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
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APPLICATION NUMBER: 60/191,078
                                                         :|:||:|:||
217 RGADYSLRAVRMKIRPLVTQ 236
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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50.0%;
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Forsyth, R.
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Best Local Similarity 50.v.
The 10; Conservative
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Carr, Grant
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US-10-112-527-1
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Sequence 2, Application US/1011257;
Sequence 2, Application NO: US20020168722A1;
Sequence 2, Application NO: US2002016872A1;
Sequence 2, Application NO: US2002016872A1;
APPLICANT: Grieninger, Gerd
APPLICANT: Appleagate, Dianne
APPLICANT: Stoke-Steben, Lara
TITLE OF INVENTION: NO: US20020168722A1e1 Cleaved Fragments of Fibrinogen
FILE REFERENCE: Docket 454-24 CON
CURRENT APPLICATION NUMBER: US/10/112,527
CURRENT FILING DATE: 2002-03-29;
PRIOR APPLICATION NUMBER: US 09/373,157
PRIOR APPLICATION NUMBER: US 09/373,157
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
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APPLICANT: Applegate, Dianne
APPLICANT: Stoike-Steben, Lara
APPLICANTON: No. US20020188722A1e1 Cleaved Fragments of Fibrinogen
FILE REFRENCE: Docket 454-24 CON
CURRENT APPLICATION NUMBER: US/10/112,527
PRIOR APPLICATION NUMBER: US 09/373,157
PRIOR FILING DATE: 1999-08-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
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Pred. No. 20;
4; Mismatches 6; Indels
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44.0%; Score 51; DB 13;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 10; Conservative 4; Mismatches 6.
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202 RGADYSLRAVRMKIRPLVTQ 221
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Publication No. US20020168722A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 126
SOFWRARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 217
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198 GSTYSLKRVEMKIRP 212
                                                                                                                                                                                                                                                                                            2 GSWYSMRKMSMKIRP 16
                                                                                                                                                                                          Query Match
Best Local Similarity 60.01
Matches 9; Conservative
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Best Local Similarity 50.0
Matches 10; Conservative
                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-112-527-3
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LENGTH: 236
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US-10-112-527-3
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APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Markus
APPLICANT: Zelder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Kropper, Burkhard
APPLICANT: Kropproge, Corinna
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: Genes coding for DNA replication and pathogenesis proteins
FILE REFERENCE: BGI-168US
CURRENT APPLICATION NUMBER: US/10/494,674
FRIGH APPLICATION NUMBER: PCT/EP02/12132
PRIOR FILING DATE: 2004-05-04
PRIOR FILING DATE: 2002-10-31
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                                                                                                                                       44.0%; Score 51; DB 13; Length 847; 50.0%; Pred. No. 62; 6; Indels ive 4; Mismatches 6; Indels
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: JP 90/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 6894, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: DE 10154246
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828 RGADYSLRAVRMKIRPLVTQ 847
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OCHIAI, KBIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKHIRO
IKEDA, MAKATO
OZAKI, AKIO
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                                                                                                                                                                                                         Conservative
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ANDO, SEIKO
      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-527-4
                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
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APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
TITLE OF INVENTION: EXPORT and modification of (poly)peptide in the lantibiotic way
CURRENT APPLICATION NUMBER: US/10/360,101
PRIOR APPLICATION NUMBER: EP 02077060.8
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.1
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 15; Length 471;
Pred. No. 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 236, Application US/10360101
Publication No. US20040009550A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Mycobacterium avium
US-10-282-122A-62157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SWYSMRKMSMKIRP 16
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US-10-360-101-236
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LENGTH: 831
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APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Rothenberg, Mark E.
TITLE OF INVENTION: NO. US2004030110Alel Proteins and Nucleic Acids Encoding Same FILE REFERENT APPLICATION NUMBER: US/10/114,270
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281,366
PRIOR APPLICATION NUMBER: 60/281,366
PRIOR PLING DATE: 2001-04-05
PRIOR PLING DATE: 2001-04-06
PRIOR PLING DATE: 2001-04-06
PRIOR PLING DATE: 2001-04-06
PRIOR PLING DATE: 2001-04-10
PRIOR PLING DATE: 2001-04-10
PRIOR PLING DATE: 2001-04-10
PRIOR PLING DATE: 2001-04-10
PRIOR PLING DATE: 2001-04-12
PRIOR PLING DATE: 2001-04-12
PRIOR PLING DATE: 2001-04-13
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42.2%; Score 49; DB 15; Length 2017;
Best Local Similarity 47.4%; Pred. No. 2.7e+02;
Matches 9; Conservative 1; Mismatches 9; Indels C
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Publication No. US20040126758A1
GENERAL INFORMATION
APPLICANT: GENERAL MARX
TITLE OF INVENTION: NOVEL HAPTOTACTIC PEPTIDES
FILE REFERENCE: 10/181,187
CURRENT FILING DATE: 2003-10-20
PRIOR APPLICATION NUMBER: US09/487790
PRIOR APPLICATION NUMBER: US09/487790
PRIOR APPLICATION NUMBER: US09/487790
PRIOR APPLICATION NUMBER: US09/487790
PRIOR PILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 6
LENGTH: 8
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                                      Gerlach, Valerie
Padigaru, Muralidhara
Shimkets, Richard A.
Gangolli, Esha A.
Taupier Jr., Raymond J.
Casman, Stacie J.
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       Catherine E.
                                                                                                                                                                                                                                                                                                                                       Rastelli, Luca
Edinger, Shlomit R.
                                                                                                                                                                                                                                                                        Anderson, David W.
Liete, Mario W.
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; ORGANISM: Homo sapiens
US-10-114-270-86
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US-10-181-187D-6
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Sequence 260795, Application US/10424599

Publication No. UG20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rose Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy N
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                                                                                                                                                                                                                                                                        Length 1646;
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43.1%; Score 50; DB 15; Length 844;
Best Local Similarity 56.2%; Pred. No. 87;
Matches 9; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                       6, Indels
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CTHER INFORMATION: Clone ID: PAT_MRT3847_77520C.1.pep
US-10-424-599-260795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1300 KISWDSNLKMSLSRGDTFSFDPSSIQMSLYRPFPPQQ 1336
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Pred. No. 1.1e+02;
1; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: ungure
LOCATION: (1)..(844)
OTHER INFORMATION: ungure at all Xaa locations
                                                                                                                              ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-494-674-46
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; Sequence 86, Application US/10114270
; Publication No. US20040030110A1
; GENERAL INFORMATION:
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APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Patturajan, Meera
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Gorman, Linda
Shenoy, Suresh G.
Pena, Carol E.A.
Smithson, Glennda
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786 GSYLTLEKMEMMIRPF 801
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Best Local Similarity 37.8%;
Matches 14; Conservative
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Gusev, Vladimir Y.
Li, Li
PRIOR FILING DATE: 2001-11-05
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                            NUMBER OF SEQ ID NOS: 96
SEQ ID NO 46
LENGTH: 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
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US-10-424-599-260795
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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sequence 30, Application US/10298461

sequence 30, Application US/10298461

publication No. US20030215451A1

general information:

APPLICANT: Ferrara, Napoleone

APPLICANT: Gerber, Hans-Peter

APPLICANT: Gerber, Hans-Peter

APPLICANT: Gerber, Maria Teresa

APPLICANT: Sherman, Daniel Eric

TITLE OF INVENTION: USING ANGIOGENIC FACTOR ANGIOPOIETIN-LIKE PROTEIN 3 ANGPTL3

FILE REFERENCE: GENERY .086A

TITLE OF INVENTION: USING ANGIOGENIC FACTOR ANGIOPOIETIN-LIKE PROTEIN 3 ANGPTL3

FILE REFERENCE: GENERY .086A

CURRENT FILING DATE: 2002-11-15

PRIOR APPLICATION NUMBER: 60/332,429

PRIOR PLING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30

LENGTH: 215
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Pred. No. 70;
3; Mismatches 4; Indels
                         4; Indels
  Best Local Similarity 56.2%; Pred. No. 7.7; Matches 9; Conservative 3; Mismatches
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Sequence 24, Application US/09832355A

Publication No. US20030027751A1

GENERAL INFORMATION:
APPLICANT: Kowesdi, Imre
APPLICANT: Kossler, Paul
FILE REFERENCE: 205654

CURRENT APPLICATION NUMBER: US/09/832,355A

CURRENT PILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 126

SOFTWARE: PatentIn version 3.0
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US-09-832-355A-21
; Sequence 21, Application US/09832355A
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201 RGGAYSLRKAAMLIRP 216
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56.2%;
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                                                                     1 KGSWYSMRKMSMKIRP
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Best Local Similarity 56.2
Matches 9; Conservative
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Best Local Similarity 56.2
Matches 9; Conservative
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ORGANISM: Homo sapiens
US-09-832-355A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                 RESULT 39
US-10-298-461-30
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                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gerber, Hans-Peter
APPLICANT: Gerber, Hans-Peter
APPLICANT: Kowalski, Joe
APPLICANT: Kowalski, Joe
APPLICANT: Sherman, Daniel Eric
TITLE OF INVENTION: COMPOSITION COMPRISING AND METHOD OF
TITLE OF INVENTION: USING ANGIOGENIC FACTOR ANGIOPOIETIN-LIKE PROTEIN 3 ANGPTL3
FILL REPERENCE: GENENT .086A
CURRENT PALLCATION NUMBER: US/10/298,461
CURRENT PILLOATION NUMBER: 60/332,429
PRIOR PILLING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
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                                         FEATURE:
; OTHER INFORMATION: Equivalent to the c-terminus of fibrinogen beta-chain
US-10-181-187D-6
                                                                                                                                                                                   Gaps
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; OTHER INFORMATION: Equivalent to the c-terminus of angiopoietin-2
US-10-181-187D-3
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                                                                                                                                  Query Match 40.5%; Score 47; DB 16; Length 8; Best Local Similarity 100.0%; Pred. No. 1.5e+06; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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; GRENERAL INFORMATION:
   APPLICANT: GERARD MARX
APPLICANT: RAPHAEL GORODETSKY
   TITLE OF INVENTION: NOVEL HAPTOTACTIC PEPTIDES
   FILE REPERENCE: 10/181,187
CURRENT APPLICATION NUMBER: US/10/181,187D
   CURRENT FILING DATE: 2003-10-20
   PRIOR APPLICATION NUMBER: US/09/487790
   PRIOR FILING DATE: 2000-01-20
   NUMBER OF SEQ ID NOS: 12
   SOFTWARE: Patentin version 3.1
   SEQ ID NO 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
40.5%; Score 47; DB 1
Best Local Similarity 69.2%; Pred. No. 6.6;
Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.5%; Score 47;
                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/10298461
Publication No. US20030215451A1
GENERAL INFORMATION:
TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
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US-10-298-461-10
                                                                                                                                                                                                                           1 KGSWYSMR 8
                                                                                                                                                                                                                                                       1 KGSWYSMR 8
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US-10-181-187D-3
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LENGTH: 16
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APPLICANT: Walanabe, Colin K.
APPLICANT: Williams, P.Mickey
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
TILL OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
TILL OF INVENTION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-08-16
PRIOR PELING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-20
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PPLICATION NUMBER: US 60/220,664
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR PLING DATE: 2000-08-23
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                                                                                         Score 47; DB 14; Length 342;
Pred. No. 1.1e+02;
3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/10223085; Publication No. US20030100497A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
                                                                                                                                                                                                                                                      324 RGGAYSLRKAAMLIRP 339
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452 RGGAYSLRKAAMLIRP 467
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Wood, William I.
Williams, P.Mickey
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                                                                                           Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 40.5
Best Local Similarity 56.2
Matches 9; Conservative
           ; ORGANISM: Homo sapiens
US-10-351-161A-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan, James
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ORGANISM:
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US-10-351-161A-48

i Sequence 48 Application US/10351161A

j Fublication No. US20030228659A1

j GENERAL INFORMATION:
    APPLICANT: Ballinger, Dennis
    APPLICANT: Montgomery, Julie
    TITLE OF INVENTION: No. US20030228659A1e1 Angiopoietin Materials and Methods
    TITLE CARENCE: 28110/35663CON
    FILE REPERENCE: 28110/35663CON
    CURRENT APPLICATION NUMBER: US/10/351,161A
    FRIOR FILING DATE: 1999-07-16
    NUMBER OF SEQ ID NOS: 48
    SEQ ID NOS: 48
    SEQ ID NO 48
    LENGTH: 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 46, Application US/10351161A
Publication No US20030228659A1
GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Mantgamery, Julie
APPLICANT: Montgamery, Julie
TITLE OF INVENTION: No. US20030228659A1e1 Angiopoietin Materials and Methods
TITLE OF INVENTION: No. US20030228659A1e1 Angiopoietin Materials and Methods
CURRENT APPLICATION NUMBER: US/10/351,161A
PRIOR APPLICATION NUMBER: US/354,881
PRIOR FILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 48
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40.5%; Score 47; DB 14; Length 279;
Best Local Similarity 56.2%; Pred. No. 88;
Matches 9; Conservative 3; Mismatches 4; Indels
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Koveedi, Imre
TITLE OF INVENTION: VEGF FUSION PROTEINS
FILE REFERENCE: 205654
CURRENT APPLICATION NUMBER: US/09/832,355A
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin version 3.0
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US-09-832-355A-21
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Best Local Similarity
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LENGTH: 279
TYPE: PRT
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LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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APPLICANT: Ye, Weillan

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIGGENESIS
FILE REFERENCE: P23.5PLC6
CURRENT APPLICATION NUMBER: US/10/23,088
FURN PELING DATE: 2002-08-16
PRIOR PELING DATE: 2002-06-36
PRIOR PELING DATE: 2000-06-23
PRIOR PELING DATE: 2000-06-23
PRIOR PELING DATE: 2000-06-23
PRIOR PELING DATE: 2000-07-26
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR APPLICATION NUMBER: US 60/220,695
PRIOR APPLICATION NUMBER: US 60/220,695
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR PELING DATE: 2000-07-28
PRIOR PELING DATE: 2000-07-28
PRIOR PELING DATE: 2000-08-17
PRIOR PELING DATE: 2000-08-23
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SEQ ID NO 4
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
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Gurney, Austin L.
Hillan, Kenneth J.
Marsters, Scot A.
Pan, James
Stephan, Jean-Philippe F.
Watanabe, Colin K.
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Watanabe, Colin K.
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; Publication No. US20030105013A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| ||:|| :| || || 452 RGGAYSLRKAAMLIRP 467
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                                                                                                                                                                                                                         Williams, P.Mickey
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APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
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Williams, P.Mickey
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Best Local Similarity 56.2
Matches 9, Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT:
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APPLICANT:
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APPLICANT: Weilan P.Mickey
APPLICANT: Ye, Weilan
APPLICANT: Ye, Weilan
APPLICANT: Ye, Weilan
APPLICANT: Ye, Weilan
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235PLC5
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR PILING DATE: 2000-06-29
PRIOR PILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-08-02
PRIOR PILING DATE: 2000-08-02
PRIOR PILING DATE: 2000-08-17
PRIOR PILING DATE: 2000-08-23
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-23
PRIOR PILING DATE: 2000-08-23
PRIOR PILING DATE: 2000-08-24
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Watanabe, Colin K.
Wood, William I.
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Publication No. US20030105012A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Mary E.
APPLICANT: Goddard, Audrey
                                                              Sequence 4, Application US/10223084
Publication No. US20030105011A1
GENERAL INFORMATION:
                                                                                                                                                       APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
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452 RGGAYSLRKAAMLIRP 467
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; ORGANISM: Homo sapiens
US-10-223-084-4
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LENGTH: 470
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US-10-223-088-4
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICATION NUMBER: US 60/220, 664

RFILING DATE: 2000-07-25

RAPPLICATION NUMBER: US 60/220, 664

RAPLICATION NUMBER: US 60/22, 695

RAPLICATION NUMBER: US 60/22, 695

RAPLICATION NUMBER: US 60/22, 695

RELING DATE: 2000-08-17

RAPLICATION NUMBER: US 9/643, 657

RELING DATE: 2000-08-17

RAPLICATION NUMBER: PCT/US00/23328

RAPLICATION NUMBER: PCT/US00/23328

RELING DATE: 2000-09-24

RELING DATE: 2000-09-18

RAPLICATION NUMBER: US 60/242,922

RELING DATE: 2000-09-18

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RAPELICATION NUMBER: PCT/USOU/30533

R FILING DATE: 2000-11-08

R FILING DATE: 2000-11-10

R FILING DATE: 2000-12-01

R APPLICATION NUMBER: PCT/USOU/3678

R APPLICATION NUMBER: US 09/747, 259

R APPLICATION NUMBER: PCT/USOU/34956

R APPLICATION NUMBER: PCT/USOU/34956

R APPLICATION NUMBER: PCT/USOU/34956

R FILING DATE: 2001-01-22

R APPLICATION NUMBER: US 09/767, 609

R FILING DATE: 2001-02-28

R APPLICATION NUMBER: PCT/USOI/06520

R FILING DATE: 2001-02-28

R APPLICATION NUMBER: PCT/USOI/06666

R APPLICATION NUMBER: PCT/USOI/06666

R APPLICATION NUMBER: PCT/USOI/06666

R FILING DATE: 2001-02-28
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R FILING DATE: 2001-03-09
R PELLING DATE: 2001-03-09
R PELLING DATE: 2001-03-14
R APPLICATION NUMBER: US 09/816,744
R APPLICATION NUMBER: US 09/828,366
R FILING DATE: 2001-04-05
R FILING DATE: 2001-04-05
R APPLICATION NUMBER: US 09/854,208
R FILING DATE: 2001-05-10
R APPLICATION NUMBER: US 09/854,208
R APPLICATION NUMBER: US 09/854,208
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FILING DATE: 2001-05-25
APPLICATION NUMBER: US 09/866,034
FILING DATE: 2001-05-25
APPLICATION NUMBER: PCZ/US01/17092
FILING DATE: 2001-05-25
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APPLICATION NUMBER: PCT/US01/21735
FILING DATE: 2001-07-09
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FILING DATE: 2001-05-30
APPLICATION NUMBER: PCT/US01/17443
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APPLICATION NUMBER: PCT/US01/17800
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APPLICATION NUMBER: PCT/US01/19692
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APPLICATION NUMBER: PCT/US01/21066
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  FILE REFERENCE: P335PIC.

CURRENT APPLICATION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

CURRENT APPLICATION NUMBER: US/10/223,090

CURRENT FILING DATE: 2002-08-16

PRIOR PLICATION NUMBER: US 60/213,637

PRIOR FILING DATE: 2000-06-23

PRIOR PLICATION NUMBER: US 60/219,556

PRIOR PLICATION NUMBER: US 60/219,556

PRIOR PLICATION NUMBER: US 60/220,624

PRIOR PLICATION NUMBER: US 60/220,644

PRIOR PLILING DATE: 2000-07-25

PRIOR PLILING DATE: 2000-08-27

PRIOR PLILING DATE: 2000-08-27

PRIOR PLILING DATE: 2000-08-21

PRIOR PLILING DATE: 2000-08-24

REMAINING PLICATION NUMBER: PCT/USO0/23328

PRIOR PLING PLICATION NUMBER: PCT/USO0/23328

PRIOR PLING PLICATION NUMBER: PCT/USO0/23328

PRIOR PLING PAIC APPLICATION DATE: 2000-08-24
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APPLICANT: Wood, William I.
APPLICANT: Williams, P.Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: COMPOSITIONS PISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C4
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
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40.5%; Score 47; DB 14; Length 470;
Best Local Similarity 56.2%; Pred. No. 1.4e+02;
Matches 9; Conservative 3; Mismatches 4; Indels
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CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR PLILNG DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR APPLICATION NUMBER: US 60/219,556
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Stephan, Jean-Philippe F.
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Publication No. US20030109438A1
GENERAL INFORMATION:
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Gerber, Hanspeter
Geritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
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ORGANISM: Homo sapiens
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APPLICANT:
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CURRENT PILIGN DATE: 2002-08-16

PRIOR APPLICATION NUMBER: US 10/091,056

PRIOR FILING DATE: 2000-02-20

PRIOR APPLICATION NUMBER: US 60/213,637

PRIOR APPLICATION NUMBER: US 60/219,556

PRIOR APPLICATION NUMBER: US 60/220,624

PRIOR PILING DATE: 2000-07-25

PRIOR FILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PILING DATE: 2000-07-25

PRIOR PELICATION NUMBER: US 60/220,664

PRIOR APPLICATION NUMBER: PCT/US00/20710

PRIOR APPLICATION NUMBER: US 60/22,695

PRIOR FILING DATE: 2000-08-28

PRIOR FILING DATE: 2000-08-28

PRIOR FILING DATE: 2000-08-28

PRIOR PELICATION NUMBER: US 60/22,695

PRIOR PELICATION NUMBER: PCT/US00/2352

PRIOR PELICATION NUMBER: PCT/US00/2352

PRIOR PELICATION NUMBER: PCT/US00/2352

PRIOR PELICATION NUMBER: PCT/US00/2352

PRIOR FILING DATE: 2000-08-17

PRIOR FILING DATE: 2000-08-14

PRIOR FILING DATE: 2000-08-24

**Remaining Prior Application data removed - See File Wrapper or PALM.

PUNDER: NUMBER: OF SEQ ID NOS: 383
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APPLICANT: Ye, Wellan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3225F1C8
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Publication No. US20030119112A1
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APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
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NUMBER OF SEQ ID NOS: 383
SEQ ID NO 4
                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-087-4
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ORGANISM: Homo sapiens
US-10-223-083-4
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CURRENT APPLICATION NUMBER: US 10/081,056
FRIOR PILING DATE: 2002-08-16
FRIOR PILING DATE: 2000-06-23
FRIOR PILING DATE: 2000-06-23
FRIOR PILING DATE: 2000-07-26
FRIOR FILING DATE: 2000-07-26
FRIOR FILING DATE: 2000-07-26
FRIOR FILING DATE: 2000-07-25
FRIOR FILING DATE: 2000-07-25
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FRIOR FILING DATE: 2000-08-27
FRIOR FILING DATE: 2000-08-27
FRIOR PLING DATE: 2000-08-24
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
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Job time : 148 secs
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                                                                                                                                                                                                                             ; Sequence 4, Application US/10223089; Publication No. US20030125521A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
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452 RGGAYSLRKAAMLIRP 467
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Wood, William I.
Williams, P.Mickey
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Matches 9; Conservative
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119, Appl 17, Appl 18, Appl 18, Appl 19, Appl 19, Appl 19, Appl 19, Appl 10, Appl 10

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Sequence 4,
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Sequence 4, Application US/08206176

Patent No. 5639940

GENERAL INFORMATION:

APPLICANT: Garner, lan

APPLICANT: Dalrymple, Michael A

APPLICANT: Prunkard, Donna E

APPLICANT: APPLICANT: Animals

CORRESPONDENCES: 27

CORRESPONDENCES: 27

CORRESPONDENCES: 27

CORRESPONDENCES: 27

COTTY: Seattle

STATE: WA

COUNTRY: USA
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COMPUTER READABLE FORM:

MEDLIN TYPE: Floppy disk

COMFUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/206,176

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGBNT INPORMATION:

NAME: Parker, Gary E
US-09-202-08BA-19
US-08-186-269-7
US-09-167-647-7
US-09-167-647-7
US-09-167-647-1
US-09-167-6-1
US-09-167-7-1
US-09-167-7-1
US-09-167-7-1
US-09-167-7-1
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Sequence 33, Appl
Sequence 6, Appli
Sequence 27, Appl
Sequence 41, Appl
Sequence 41, Appl
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                                                                                                 January 18, 2005, 11:04:01 ; Search time 38 Seconds (without alignments) 36.649 Million cell updates/sec
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Sequence 1, Al
Sequence 28, Al
Sequence 4, Al
Sequence 1009
Sequence 19, Al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-919-039-33
US-08-919-039-33
US-08-434-099A-27
US-08-434-099A-28
US-08-434-099A-28
US-08-64-945-41
US-08-64-945-102
US-08-64-945-102
US-08-642-255-137
US-08-947-63A-47
US-08-397-633A-47
US-08-397-633A-47
US-08-397-633A-62
US-08-397-633A-62
US-08-397-633A-11
US-08-397-633A-11
US-08-397-633A-11
US-08-397-633A-11
US-08-397-633A-11
US-08-397-633A-11
US-08-397-633A-11
US-08-397-633A-11
US-08-397-633A-11
US-08-992-741B-1
US-09-912-740B-1
US-09-912-740B-1
US-09-912-740B-1
US-08-525-505A-4
US-08-525-505A-4
US-08-525-505A-4
US-08-525-505A-4
US-08-525-505A-4
US-08-525-505A-4
US-08-912-740B-1
                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                     478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                      116
1 KGSWYSMRKMSMKIRPFFPQQ 21
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                         US-09-487-790A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
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                                                                                                                                                                                                        Sequence:
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                                                                                                           Run on:
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No.
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51.7%; Score 60; DB 1; Length 453; 64.7%; Pred. No. 0.066;
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US-08-434-099A-27
Sequence 27, Application US/08434099A
Fatent No. 6083902
GENERAL INFORMATION:
TITLE OF INVENTION: Recombinant Fibrin Chains,
TITLE OF INVENTION: Ribrin and Fibrin-Homologs
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE E.R. Squibb & Sons, Inc.
STREET: 100 Headquarters Park Drive
CITY: Skillman
                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKELEE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASELSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,099A
FILING DATE: 03-MAY-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,979
FILING DATE: 02-MAY-1994
ATTORNEY AGENT INPORMATION:
NAWE: FURMAN, UK: BSQ., Theodore R
REGISTRATION NUMBER: 30,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 KTRWYSMKKTTMKIIPF 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KGSWYSMRKMSMKIRPF 17
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TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
                                                                                                                                                                                                                                                                                         TELEPHONE: 206-547-8080 ex
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acids
                                                                                                                                                                                                                                                                                                                                                                       : 453 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 454 amino acids
amino acid
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
          COMPUTER READABLE FORM:
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                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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Patent No. 5639940

GENERAL INFORMATION:
APPLICANT: Garner, lan
APPLICANT: Prunkard, Donna E
APPLICANT: Production of Fibrinogen in Transgenic
TITLE OF INVENTION: Animals
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
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100.0%; Score 116; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 21; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.4%; Score 113; DB 4; Length 488; 95.2%; Pred. No. 1e-10; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 3393861CD1
US-09-919-039-33
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMONINICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEPAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                             471 KGSWYSMRKMSMKIRPFFPQQ 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468 KGSWYSMKKWSWKIRPFFPQQ 488
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Matches 20; Conservative
                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: WA
COUNTRY: USA
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US-09-919-039-33
                                                                                                                                                                                                                              US-08-206-176-4
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Gaps

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APPLICANT: Matti Sallberg

TITLE OF INVENTION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS

TITLE OF INVENTION: THAT REDIRECT ANTIBODIES TO RECEPTORS ON A PATHOGEN

FILE REPERENCE: TRIPEP.00709-945

CURRENT APPLICATION NUMBER: US/09/664,945

PRIOR APPLICATION NUMBER: US/09/52,106

PRIOR APPLICATION NUMBER: US/246,258

PRIOR FILING DATE: 1999-02-08

PRIOR FILING DATE: 1999-02-08

PRIOR FILING DATE: 1999-02-08

PRIOR FILING DATE: 1996-12-27

PRIOR FILING DATE: 1994-04-28

NUMBER OF SEQ ID NOS: 105

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 41

LENGTH: 20
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Sequence 37, Application US/08397633A

Sequence 37, Application US/08397633A

Patent No. 5713510:
GENERAL INFORMATION:
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
TITLE OF INVENTION: OF BNZYMATIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: PLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CALLILLIANDER
COUNTRY: USA
ZIP: 9411-1487
ZIP: 9411-1487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenefin Release #1.0, Version #1.25
SOFTWARE: Patenefin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND BERTE: 20,015
REFERENCE/DOCKET NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A.58848-1/BIR PROP-011-1
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SHOW INFORMATION:
TELECOMUNICATION SHOW INFORMATION:
TELECOMUNICATION OF SEQ 1D NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TVORE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
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Pred. No. 0.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Specificity domain peptide US-09-664-945-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 WYSMKKTTMKIIPF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 71.4*
Matches 10; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                   Length 454;
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                                                                                                                                                                                                                                                                               4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/08434099A
; Sequence 28, Application US/08434099A
; Patent NO. 6083902
; GENERAL INFORMATION:
; APPLICANT: Cederholm-Wms., Stewart A.
TITLE OF INVENTION: Fibrin and Fibrin-Homologs; TITLE OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.R. Squibb & Sons, Inc.
; STREET: 100 Headquarters Park Drive
; CITY: SAilman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Disketter
COMPUTER: DISKette
                                                                                                                                                                                                             Query Match 51.7%; Score 60; DB 3; Best Local Similarity 64.7%; Pred. No. 0.066; Matches 11; Conservative 2; Mismatches
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Pred. No. 0.066;
2; Mismatches
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; Sequence 41, Application US/09664945
; Patent No. 6660842
; GRNERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
US-08-434-099A-28
                                                                                                                                                                                                                                                                                                                                                                                  416 KTRWYSMKKTTMKIIPF 432
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-281-2372
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Best Local Similarity 64.7%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 908-281-2373
                                                 TOPOLOGY: linear — MOLECULE TYPE: protein FRAGMENT TYPE: internal
                   STRANDEDNESS: Bingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                          ; FRAGMENT TYPI
US-08-434-099A-27
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STATE: N.
COUNTRY:
ZIP: 085
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1S-08-397-633A-38
Sequence 38, Application US/08397633A
Sequence 38, Spring Sequence 38, Sequence 38, Sequence 38, Sequence 38, Spring S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 73;
0.02;
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ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDTUM TYPE: Elloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A-58848-1/BIR PROP-011-1
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Best Local Similarity 71.4%; Pred. No. 0.02;
Matches 10; Conservative 2; Mismatches
                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETLYAM I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A5556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8701
TELEFAX: (10 277299 FHT UR
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: FLEHR, HOHBACH, TEST, ALBRITTO
4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 58;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETTEAM I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: (415) 781-1989
TELEPAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 WYSMKKTTMKIIPF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide US-08-642-255-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4 Embarcader
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Patent No. 660842

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Matti Sallberg

TITLE OF INVENTION:
FILE REPERENCE:
TRIPEPO 007CP3

CURRENT FILING DATE: 2000-09-19

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 1999-02-08

PRIOR FILING DATE: 1999-02-08

PRIOR FILING DATE: 1999-02-08

PRIOR FILING DATE: 1999-02-08

PRIOR FILING DATE: 1994-04-28

NUMBER OF SEQ ID NOS: 105

SOFFWARE: FEASTERQ for Windows Version 4.0

LENGTH: 27
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; Sequence 127, Application US/08642255
; Patent No. 5773249
; Patent No. 5773249
; PAPLICANT: CAPPELLO, Joseph
; APPLICANT: CAPPELLO, Joseph
; APPLICANT: FERRARI. Franco. A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; TITLE OF INVENTION: High Molecular Weight Collagen-Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 58; DB 4; Length 21;
Pred; No. 0.0069;
2; Indels
                                                                            Score 58; DB 1; Length 21;
Pred. No. 0.0053;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2: Mismatches
                                                                        50.0%;
illarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 50.0%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                  4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                 3 WYSMKKTTMKIIPF 16
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                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
US-08-397-633A-37
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Sequence 131, Application US/08642255
; Patent No. 577249
; GENERAL INFORMATION:
; APPLICANT: CAPPELLO, Joseph
; APPLICANT: PERRARI, Franco A.; TITLE OF INVENTION: High Molecular Weight Collagen-Like; TITLE OF INVENTION: Protein Polymers
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLERR, HOHBACH, TEST, ALBRITTON & HERBERT; CAREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 75;
COMPUTER RADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROALLand, Bettram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 398-3249
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
TELERX: 910 277299
INFORMATION FOR SEG ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

FLING DATE:

CLASSIFICATION NUMBER: US/08/642,255

ATTORNEY/AGENT INFORMATION:

NAME: ROWLAND, Bertram I.

REGISTRATION NUMBER: A5556-3/BIR

REGISTRATION NUMBER: A5556-3/BIR

TELEPHONE: (415) 494-871

TELEPHONE: (415) 494-871

TELEFA: 910 277299 FHT UR

INFORMATION FOR EQ ID NO: 131:

SEQUENCE CHRACTERISTICS:

LENGTH: 198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58; DB Pred. No. 0.022; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.0%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 WYSMRKMSMKIRPF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-633A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-642-255-131
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Sequence 47, Application US/08397633A

Sequence No. 5773510N:

Batent No. 5773510N:

APPLICANT: Cappello. Joseph

TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE

TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING

TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING

CORRESPONDENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLERF, HOHBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

CITY: San Francisco

COUNTRY: USA
                                                                                                                                                                    Sequence 130, Application US/08642255
; Batent No. 5773249
; GENERAL INFORMATION:
   APPLICANT: CAPPELLO, Joseph
   APPLICANT: FERRALI, Franco A.
   TITLE OF INVENTION: High Molecular Weight Collagen-Like
   TITLE OF INVENTION: Protein Polymers
   NUMBER OF SEQUENCES: 135
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
   STREET: 4 Embarcadero Center, Suite 3400
   CITY: San Francisco
   STATE: California
   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58; DB 1; Length 75;
Pred. No. 0.021;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/ACENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 455556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELEFAX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 130:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
            4 WYSMRKMSMKIRPF 17
                                         35 WYSMKKTTMKIIPF 48
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LENGTH: 75 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 50.0
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                         US-08-642-255-130
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Sequence 2, Application US/08525505A
Fatent No. 5807711
GENERAL INFORMATION:
APPLICANT: HARA, HIROSHI
APPLICANT: WATSUKI, YUMIKO
APPLICANT: MATSUKI, YUMIKO
APPLICANT: HANADA, KAZUNORI
TITLE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58; DB 1; Length 198; Pred. No. 0.059; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 4-58848-1/BIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 101-1989
TELERAX: 910 277299
INFORMATION FOR SEC 1D NO: 52:
SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/525,505A
FILING DATE: 22-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                         ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 198 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 WYSMKKTTMKIIPF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-525-505A-2
                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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0
                                                                                                                                                                                                                                                                                                                                                              | Sequence 41, Application US/08397633A |
| Patent No. 5773577 |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: Cappello, Joseph |
| TITLE OF INVENTION: | PRODUCTS COMPRISING SUBSTRATESCAPABLE |
| TITLE OF INVENTION: | OF ENZYMATIC CROSS-LINKING |
| NUMBER OF SEQUENCES: 105 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT |
| STREET: | 4 Embarcadero Center, Suite 3400 |
| COUNTRY: California |
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-397-633A-52
; Sequence 52, Application US/08397633A
; Patent No. 5773577;
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
                                                                                                                                        Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 198
                                                                                                                                                                                2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROWLING, BETTRAIL
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1989-1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
                                                                                                                                     Score 58; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58; DB 1;
Pred. No. 0.059;
2; Mismatches
                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELERAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                   Query Match 50.0%;
Best Local Similarity 71.4%;
Matches 10; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.0%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                        4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                4 WYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                           US-08-642-255-131
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Gaps

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US-08-748-150-1

Sequence 1, Application US/08748150

Sequence 1, Application US/08748150

Patent No. 5919754

GENERAL INFORMATION:

APPLICANT: Altieri, Dario C

APPLICANT: Thornton, George B

TITLE OF INVENTION: ENDOTHELIAL CELL AND FIBRINOGEN MEDIATED INFLAMMATION

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: The SCIIDER Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10666 No. 5919754th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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                                                                                                                                                      LOCATION: 88
OTHER INFORMATION: /note= "SITE OF GLYCOSYLATION"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Pacerial Roleage #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/748,150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REPERENCE/DOCKET NUMBER: SCR 300.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/232,532
FILING DATE: 25-APR-1994
APPLICATION NUMBER: US 08/139,562
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,117
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: La Jolla
STATE: CA
COUNTR: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 KTRWYSMKKTIMKIIPF 389
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                                                                                                                                                                                                                               Disulfide-bond
153..182
                                                                                                                                                                                                                                                                                                          Disulfide-bond 326..339
                                                                                                                              NAME/KEY: Modified-site
                                                MOLECULE TYPE: protein FEATURE:
                          TYPE: amino acid
TOPOLOGY: linear
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TOPOLOGY: linear
                                                                                                                                                                                                       FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                       , NAME/KEY;
, LOCATION:
US-08-232-532-1
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Sequence 1, Application US/08232532
Patent No. 559730
GENERAL INFORMATION:
APPLICANT: Altieri, Dario C
APPLICANT: Thornton, George B
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
TITLE OF INVENTION: ENDOTHELIAL CELL AND FIBRINGGEN MEDIATED INFLAMMATION
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5599790th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: EN PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/23,532
FLING DATE: 25-APR-1994
PRIOR APPLICATION NUMBER: US 08/139,562
FILING DATE: 19-OCT-1993
PRIOR APPLICATION NUMBER: US 08/139,562
FILING DATE: 11-OUT-1993
ATPLICATION NUMBER: US 07/898,117
FILING DATE: 11-JUN-1992
ATPLICATION NUMBER: US 07/898,117
FILING DATE: 11-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                 4587-012-0 PCT
                APPLICATION NUMBER: PCT/JP94/00455
FILING DATE: 22-MAR-1994
PRIOR APPLICATION DATA: 994
APPLICATION NUMBER: JP 05-063905
FILING DATE: 23-MAR-1993
ATTORNEY-AGENT INFORMATION:
NAME: OBLON, NORWAN F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,018
REGISTRATION STATE NORWATION:
TELEPHONE: 703-413-220
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH 314 amino acide
TYPE: AMINO acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCR 300.1
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REGISTRATION NUMBER: 34,163
REFRENCE/DOCKET NUMBER: SCR.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 52.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
PRIOR APPLICATION DATA:
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US-08-232-532-1
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Sequence 1, Application US/09912740A

Sequence 1, Application US/09912740A

Patent No. 6676940

GRERAL INFORMATION:
APPLICANT: Altieri, Dario C

APPLICANT: Languino, Lucia R

APPLICANT: Tanguino, Lucia R

APPLICANT: Tanguino, Lucia R

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING

TITLE OF INVENTION: ENDOTHELIAL CELL AND FIBRINOGEN MEDIATED INFLAMMATION

TITLE OF INVENTION: ENDOTHELIAL CELL AND FIBRINOGEN MEDIATED INFLAMMATION

TITLE OF INVENTION: WINDER: US/09/912, 740A

CURRENT APPLICATION NUMBER: US 09/347,877

PRIOR FILING DATE: 1999-07-06

PRIOR FILING DATE: 1999-07-06

PRIOR APPLICATION NUMBER: US 08/139,562

PRIOR APPLICATION NUMBER: US 08/139,562

PRIOR FILING DATE: 1993-10-19

PRIOR FILING DATE: 1993-10-19

PRIOR FILING DATE: 1993-06-12

PRIOR FILING DATE: 1993-06-12

PRIOR FILING DATE: 1993-06-12

PRIOR FILING DATE: 1993-06-12

SOSTWARR OF SEQ ID NOS: 5

SOSTWARR PRIOR DATE: 1993-06-12
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                                                                                                                                                                              DB 3; Length 411;
                                                                                                                                                                                                                          5; Indels
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                                                                                                                                                                         Query Match 49.1%; Score 57; DB 3; Best Local Similarity 64.7%; Pred. No. 0.19; Matches 11; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 49.1%; Score 57; DB 4; Best Local Similarity 64.7%; Pred. No. 0.19; Matches 11; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CARBOHYD
LOCATION: 88
OTHER INFORMATION: site of glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: DISULFID
LOCATION: (153)...(182)
OTHER INFORMATION: disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (326)...(339)
CTHER INFORMATION: disulfide-bond
US-09-912-740A-1
                                                                                                                                                                                                                                                                                              373 KTRWYSMKKTIMKIIPF 389
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                      Disulfide-bond
                                                                                       Disulfide-bond
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                                                153..182
                                                                                                              326..339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Unknown
                    NAME/KEY:
LOCATION:
FEATURE:
                                                                                       , NAME/KEY:
, LOCATION:
US-09-347-877-1
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US-09-912-741B-1
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Betent No. 626549

GENERAL INFORMATION:
APPLICANT: Altieri, Dario C
APPLICANT: Languino, Lucia R
APPLICANT: Thornton, George B
TITLE OF INVENTION: ENDOTHELIAL CELL AND FIBRINOGEN MEDIATED INFLAMMATION
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Soripps Research Institute, Office of
ADDRESSEE: The Soripps Torrey Pines Road, TPC 8
CONTRET: 10666 No. 6265549th Torrey Pines Road, TPC 8
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49.1%; Score 57; DB 2; Length 411;
Best Local Similarity 64.7%; Pred. No. 0.19;
Matches 11; Conservative 1; Mismatches 5; Indels
                                                                LOCATION: 88
OTHER INFORMATION: /note= "SITE OF GLYCOSYLATION"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 88
OTHER INFORMATION: /note= "SITE OF GLYCOSYLATION"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/347,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/232,532
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,117
FILING DATE: 11-JUN-1992
ATTORNEY/AGRAT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR 300.1
TELECHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        373 KTRWYSMKKTIMKIIPF 389
                                                                                                                                                                                                                                                                                                                                                                               1 KGSWYSMRKMSMKIRPF 17
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TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                Disulfide-bond 326..339
                                                                                                                                  NAME/KEY: Disulfide-bond
             FEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
MOLECULE TYPE: protein
                                                                                                                                                         153..182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92037
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                                                                                                                                                       LOCATION:
                                                                                                                                                                         FEATURE:
NAME/KEY:
                                                                                                                                                                                                                     ; LOCATION:
US-08-748-150-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 19
US-09-347-877-1
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STATE:
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Gaps

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Gape
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APPLICANT: Benjamin, Scepinaire
APPLICANT: Tanaka, Hiroák,
TITLE OF INVENTUON: HUMAN CONAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.USS.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-4
PRIOR FILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PLICATION NUMBER: US 60/305,456
PRIOR PLICATION NUMBER: US 60/302,277
PRIOR PLICATION NUMBER: US 60/298,698
PRIOR PLILING DATE: 2001-06-12
PRIOR PLILING DATE: 2001-06-12
PRIOR PLILING DATE: 2001-06-15
PRIOR PLILING DATE: 2001-06-15
PRIOR PLILING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR PLING DATE: 2001-06-15
PRIOR PLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR APPLICATION NUMBER: US 60/293,574
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7
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49.1%; Score 57; DB 5; Length 411;
Best Local Similarity 64.7%; Pred. No. 0.19;
Matches 11; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 282;
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                                                                                                                                                                                    NAME/KEY: Modified-site
LOCATION: 88
OTHER INFORMATION: /note= "SITE OF GLYCOSYLATION"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.0%; Pred. No. 0.19
Matches 11; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-000-489-28
; Sequence 28, Application US/10000489
; Patent No. 6794363
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 GWWYSLKSVVMKIRPNDFIP 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GSWYSMRKMSMKIRP--FFP 19
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OTHER INFORMATION: Xaa = Asn,Thr;
NAME/KEY: UNSURE
LOCATION: 233
OTHER INFORMATION: Xaa = Phe,Ser
US-10-000-489-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 KTRWYSMKKTIMKIIPF 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KGSWYSMRKMSMKIRPF 17
                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 153..182
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
326..339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Benjanin, Stephane
                                                                                              MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   , NAME/KEY:
, LOCATION:
PCT-US95-05168-1
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               GENERAL INFORMATION:
PATENT NO. 6737058
GENERAL INFORMATION:
PAPELICANT: Altieri, Dario C
APPLICANT: Altieri, Dario C
APPLICANT: Altieri, Dario C
APPLICANT: Thornton, George B
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
TITLE OF INVENTION: MEDOTHELIAL CELL AND FIBRINGGEN MEDIATED INFLAMMATION
FILE OF INVENTION: MEDATE: US/09/912,741B
CURRENT APPLICATION NUMBER: US/09/912,741B
CURRENT PILING DATE: 1999-07-06
PRIOR FILING DATE: 1996-01-06
PRIOR FILING DATE: 1996-01-12
PRIOR PELICATION NUMBER: US 08/139,562
PRIOR FILING DATE: 1993-04-25
PRIOR FILING DATE: 1991-01-19
PRIOR FILING DATE: 1991-01-19
PRIOR FILING DATE: 1992-06-12
PRIOR PELICATION NUMBER: US 07/898,117
PRIOR FILING DATE: 1992-06-12
PRIOR PELICATION NUMBER: US 07/898,117
PRIOR FILING DATE: 1992-06-12
PRIOR FILING DATE: 1992-06-12
PRIOR FILING DATE: 1992-06-12
PRIOR PELICATION NUMBER: US 07/898,117
PRIOR FILING DATE: 1993-10-19
PRIOR PRIOR
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TITLE OF INVENTION: ENDOTHELIAL CELL AND FIBRINGEN MEDIATED INFLAMMATION
WUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Datentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05168
FILING DATE: 24-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/232,532
FILING DATE: 25-APR-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: site of glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application PC/TUS9505168
GENERAL INFORMATION:
APPLICANT:
Sequence 1, Application US/09912741B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: DISULFID

CCATION: (326)...(339)

CTHER INFORMATION: disulfide-bond

US-09-912-7418-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: DISULFID
LOCATION: (153)...(182)
OTHER INFORMATION: disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 KTRWYSMKKTIMKIIPF 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 64.77
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CARBOHYD
LOCATION: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-05168-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                       Length 312;
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                                                                                                                                                                                                                                    4; Indels
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                                                                                                    ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 029251CD1
US-09-976-594-1009
                                                                                                                                                                                     Query Match
48.3%; Score 56; DB 4;
Best Local Similarity 55.0%; Pred. No. 0.21;
Matches 11; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFRWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.1;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICAL...
FILING DATE:
CLASSIPICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130p1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEPHONE: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gorney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/09136801; Patent No. 6413770; GENERAL INFORMATION: APPLICANT: Godowski, Paul J. APPLICANT: Gurney, Austin
                                                                                                                                                                                                                                                                                                          290 GWWYSLKSVVMKIRPNDFIP 309
                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 19, Application US/08960507; Patent No. 6057435
                                                                                                                                                                                                                                                                             2 GSWYSMRKMSMKIRP--FFP 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1.4-CIBRISTICS: TYPE: Amino Acids TOPOLOGY: 1.4-CID 960-E-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 GSTYSLKRVEMKIRP 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                    LENGTH: 312
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      US-08-960-507-19
SEQ ID NO 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-960-507-19
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                                                                                   FEATURE:
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Batent No. 6673549

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR PAPLICATION NUMBER: 60/240,409
PRIOR PILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                               APPLICANT: HARA, HIROSHI
APPLICANT: YOSHIMMRA, HIROMITSU
APPLICANT: MATSUKI, YUMIKO
APPLICANT: HANDA, SAEKO
APPLICANT: HANDA, KAZUNORI
TITLE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE. V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,505A
FILING DATE: 22-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00455
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-063905
FILING DATE: 22-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-063905
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 48.3%; Score 56; DB 1;
Best Local Similarity 55.0%; Pred. No. 0.21;
Matches 11; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
           Sequence 4, Application US/08525505A Patent No. 5807711 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 GWWYSLKSVVMKIRPNDFIP 309
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TOPOLOGY: 1:----
OLECTH: ALL
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                USA
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Sequence 7. Application US/09167647

Sequence 7. Application US/09167647

Batent No. 6022476

GENERAL INFORMATION:

APPLICANT: Grieninger, Gerd

APPLICANT: Grieninger, Gerd

APPLICANT: Ahadi, Mohamad Zaher

CURRENT ELLE SEG. ID #1 - 7 454-7 DIV

CURRENT PILING DATE: 1999-10-06

EARLIER APPLICATION NUMBER: 08/479,755

EARLIER PILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 7

SOSTWARE: Patentin Ver. 2.0
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APPLICANT: Grieninger, Gerd
APPLICANT: Fu, Yiping
APPLICANT: Roo, Yan
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Rudryk, Bohdan J.
ITILE OF INVENTION: MONOSPECTFIC ANTIBODIES AGAINST A SUBUNIT OF FIBRINOGEN
FILE REPERBNCE: Sequences 1-7 fcov/CPA
CURRENT APPLICATION NUMBER: US/08/886,269
CURRENT FILING DATE: 1997-07-01
EARLIER APPLICATION NUMBER: 08/479,755
EARLIER PILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                           44.8%; Score 52; DB 4; Length 346; 60.0%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 27;
                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                           Mismatches
                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/08886269
; Patent No. 6025148
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KGSWYSMRKMSMKIRPFFPQ 20
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|8 RGADYSLRAVRMKIRPLVTQ 27
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                                                                                                                                       2 GSWYSMRKMSMKIRP 16
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Best Local Similarity 50.09
Matches 10; Conservative
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Best Local Similarity 50.0
Matches 10; Conservative
                                                                                         Conservative
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ORGANISM: Homo mapiens
US-08-886-269-7
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; ORGANISM: Homo sapiens
US-09-167-647-7
                                           Query Match
Best Local Similarity
Matches 9; Conserva
US-09-202-088A-19
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44.8%; Score 52; DB 4; Length 346;
Best Local Similarity 60.0%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 2; Indels
                                                       APPLICANT: BOUGARD, MARGATER APPLICANT: BOUGARD, MARGATER APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Schwall, Ralph TITLE OF INVENTION: Tie Ligand Homologues NUMBER OF SEQUENCES: 35 CORRESS: ADDRESSE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA CONTRY: USA CONTRY: USA ZIP: 94080 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WINBALIN (Genentech) CURRENT APPLICATION DATA: APPLICATION UNMBER: US/09/136,801 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Kenneth
APPLICANT: Botstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Roy, Margaret
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE REFERENCE: P1130910S
CURRENT APPLICATION NUMBER: US/09/202,088A
CURRENT FILING DATE: 1998-12-08
PRIOR FILING DATE: 1998-09-14
NUMBER: OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 31.055
REFERENCE/DOCKET NUMBER: P1130P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEPAX: 650/922-9881
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/09202088A Patent No. 6551822 GENERAL INFORMATION: APPLICANT: Godowski, Paul J. APPLICANT: Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 GSTYSLKRVEMKIRP 341
                     Botstein, David
Goddard, Audrey
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
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US-09-202-088A-19
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LENGTH: 346
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Sequence 3. Application US/08886269

Fatent No. 6025148

GENERAL INFORMATION:

APPLICANT: Grieninger, Gerd

APPLICANT: Grieninger, Gerd

APPLICANT: Cao, Yan

APPLICANT: Abadi, Mohamad Zaher

APPLICANT: Rudryk, Bohdam J.

TITLE OF INVENTY APPLICANTON: MONOSPECIFIC ANTIBODIES AGAINST A SUBUNIT OF FIBRINOGEN

FILE REFERENCE: Sequences 1-7 for 454-7 CON/CPA

CURRENT FILING DATE: 1997-07-01

EARLIER APPLICATION NUMBER: 08/479,755

EARLIER FILING DATE: 1995-06-07

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0
                APPLICANT: Cao, Yan
APPLICANT: Abadi, Mohamad Zaher
APPLICANT: Abadi, Mohamad Zaher
APPLICANT: Abadi, Mohamad Zaher
APPLICANT: Widryk, Woldon Bohdan J.
TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AGAINST A SUBUNIT OF FIBRINOGEN
FILE REPERENCE: Sequences 1-7 for 454-7 CON/CPA
CURRENT APPLICATION NUMBER: US/08/886, 269
CURRENT FILING DATE: 1995-07-01
EARLIER APPLICATION NUMBER: 08/479, 755
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.0
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Patent No. 6025476

GENERAL INFORMATION:
APPLICANT: Grininger, Gerd
APPLICANT: Fu, Yiping
APPLICANT: Andi, Mohamad Zaher
APPLICANT: Andi, Mohamad Zaher
APPLICANT: Rudryk, Bohdan J
TITLE OF INVENTION MONOSPECIFIC ANTIBODIES AGAINST A SUBUNIT OF FIBRINOGEN
FILE REFERENCE: Seq. ID ## 1 - 7 - 455 - 7 DIV
CURRENT APPLICATION NUMBER: US/09/167,647
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4; Mismatches
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US-08-886-269-2
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US-09-167-647-1
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US-08-886-269-1
| Sequence 1, Application US/08886269
| Patent No. 6025148
| General Information:
| APPLICANT: Grieninger, Gerd
| APPLICANT: Garieninger, Gerd
| APPLICANT: Garieninger, Gerd
| APPLICANT: Cao, Yan
| APPLICANT: Abadi, Mohamad Zaher
| APPLICANT: Abadi, Mohamad Zaher
| APPLICANT: Abadi, Mohamad Zaher
| APPLICANT: Cao, Yan
| APPLICANT: Cao, Yan
| FILE REFERENCE: Sequences 1-7 for 454-7 CON/CPA
| CURRENT APPLICATION NUMBER: 1097-07-01
| EARLIER APPLICATION NUMBER: 08/479,755
| BARLIER FILING DATE: 1995-06-07
| NUMBER OF SEQ ID NOS: 7
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                                                                                                                      Sequence 3, Application US/09373157

Patent No. 6416963

GENERAL INFORMATION:
APPLICANT: Grieninger, Gerd
APPLICANT: Appleagre, Dianne
APPLICANT: Stoike-Steben, Lara
TITLE OF INVENTION: NOVEL CLEANED FRAGMENTS OF FIBRINOGEN
FILE REFERENCE: Sequence ID No. 6416963, 1-7 for 454-24
CURRENT APPLICATION NUMBER: US/09/373,157
CURRENT FILING DATE: 1999-08-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 44.0%; Score 51; DB 4; Length 221; Best Local Similarity 50.0%; Pred. No. 0.97; Matches 10; Conservative 4; Mismatches 6; Indele
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202 RGADYSLRAVRMKIRPLVTQ 221
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217 RGADYSLRAVRMKIRPLVTQ 236
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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Best Local Similarity
Matches 10; Conserv
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                                                                                         RESULT 31
US-09-373-157-3
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US-08-886-269-2
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                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09373157
; Sequence 2, Application US/09373157
; Patent No. 6416963
; APPLICANT: Grieninger, Gerd
; APPLICANT: Grieninger, Gerd
; APPLICANT: Applegate, Dianne
; APPLICANT: Applegate, Dianne
; TILE OF INVENTION: NOVEL CLEAVED FRAGMENTS OF FIBRINOGEN
; FILE REFERENCE: Sequence ID No. 6416963. 1-7 for 454-24
; Patent No. 6416963
; CURRENT APPLICATION NUMBER: US/09/373,157
; CURRENT PILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver: 2.0
; SEQ ID NO 2:
; LENGTH: 236
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; Sequence 1, Application US/09373157
; Patent No. 6416963
; GENERAL INPORMATION:
; APPLICANT: Grieninger, Gerd
; APPLICANT: Appleate, Dianne
; APPLICANT: Stolke-Steben, Lara
; TITLE OF INVENTION: NOVEL CLEAVED FRAGMENTS OF FIBRINOGEN
; FILE REPERBNCE: Sequence ID No. 6416963: 1-7 for 454-24
; Patent No. 6416963
; CURRENT APPLICATION NUMBER: US/09/373,157
; CURRENT PILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO :
; LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51; DB 4; Length 236;
Pred. No. 1;
4; Mismatches 6; Indels
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                                                                                                                                               6; Indels
                                                                                              Query Match
44.0%; Score 51; DB 3;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 10; Conservative 4; Mismatches
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232 RGADYSLRAVRMKIRPLVTQ 251
                                                                                                                                                                                             1 KGSWYSMRKMSMKIRPFFPQ 20
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Best Local Similarity 50.0%;
Matches 10; Conservative
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Matches 10; Conservative
                             ; ORGANISM: LEPORIDAE SP.
US-09-167-647-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-09-373-157-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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       TYPE: PRT
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Sequence 4, Application US/09167647

Batent NO. 6025476

GENERAL INFORMATION:

APPLICANT: Grieninger, Gerd

APPLICANT: Ahadi, Mohamad Zaher

CURRENT APPLICATION NUMBER: US/09/167,647

CURRENT PILING DATE: 1998-10-06

EARLIER APPLICATION NUMBER: 08/479,755

EARLIER PILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Grieninger, Gerd
APPLICANT: Fu, Yiping
APPLICANT: Cao, Yan
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Kudryk, Bohdan J
TITLE OF INVENTION MONOSPECIFIC ANTIBODIES AGAINST A SUBUNIT OF FIBRINOGEN
FILE REFERENCE: Seq. ID #1 - 7 545-7 DIV
CURRENT APPLICATION NUMBER: US/09/167,647
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                              Length 236;
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                                                                                                                                                                                                                                                                                                            6; Indels
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44.0%; Score 51; DB 3;
Best Local Similarity 50.0%; Pred. No. 1;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51; DB 3;
Pred. No. 1;
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CURRENT FILING DATE: 1998-10-06
BARLIER APPLICATION NUMBER: 08/479,755
BARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 236
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217 RGADYSLRAVRMKIRPLVTQ 236
                                                                                                                                                                                                                                                                                                                                                      1 KGSWYSMRKMSMKIRPFFPQ 20
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Patent No. 6025476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0°
Matches 10; Conservative
                                                                                                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-09-167-647-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: PAPIO SP
US-09-167-647-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-167-647-2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/07654839;
Sequence 5, Application US/07654839;
Fatent No. 5372933;
GENERAL INFORMATION:
APPLICANT: Zamarron, Concepcion
APPLICANT: Plow, Edward F
APPLICANT: Plow, Edward F
APPLICANT: Ginsberg, Mark H
TITLE OF INVENTION: RCEPTOR-INDUCED BINDING SITES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5372933th Torrey Pines Road., Suite 220,
STREET: Mail Drop TPC8
COITY: La Jolla
STATE: CA
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                                                                                                                                                                                                                                                            DB 1; Length 13;
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MEDIUM TYPE: Floppy disk
COMPUTER: Eleopy disk
COMPUTER: THE PC COMPATIBLE
OPERATION SYSTEM: PC-005/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSIFICATION NUMBER: US/07/654,839
FILING DATE: 19910213
CLASSIFICATION NUMBER: US 07/252,753
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/415,029
FILING DATE: 29-SEP-1989
ATFORNEY/AGENT INFORMATION:
NAME: BINGHAM: 32,457
REGISTRATION NUMBER: 32,457
REJERRANCE/DOCKET NUMBER: 32,457
TELEPRAK: 619-554-2937
TELEPRAK: 619-554-2937
                                                                                                                                                                                                                                                        Score 48; DB 1;
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                            41.4%;
61.5%;
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
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1 KSRWYSMKKTTMK 13
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.5
Matches 8; Conservative
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NO
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NO
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HYPOTHETICAL:
US-07-654-839-9
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HYPOTHETICAL:
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; Sequence 9, Application US/07654839
; Patent No. 5372933
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Plow, Edward F
; APPLICANT: Ginsberg, Mark H
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST
TITLE OF INVENTION: RECEPTOR-INDUCED BINDING SITES
NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5372933th Torrey Pines Road., Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
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                                                    Sequence 4, Application US/09373157
Sequence 4, Application US/09373157
Sequence 4, Application US/09373157
GENERAL INNORMATION:
APPLICANT: Grieninger, Gerd
APPLICANT: Applegate, Dianne
APPLICANT: Stoike-Steben, Lara
TITLE OF INVENTION: NOVEL CLEAVED FRAGMENTS OF FIBRINOGEN
FILE REFERENCE: Sequence ID No. 6416963. 1-7 for 454-24
Patent No. 6416963
CURRENT APPLICATION NUMBER: US/09/373,157
CURRENT FILING DATE: 1999-08-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENOTH: 847
TYPE: PRT
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44.0%; Score 51; DB 4; Length 847;
Best Local Similarity 50.0%; Pred. No. 4.1;
Matches 10; Conservative 4; Mismatches 6; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOCTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/654,839
FILING DATE: 19910213
APPLICATION NUMBER: US 07/252,753
FILING DATE: 03-0CT-1988
FILING DATE: 03-0CT-1988
FILING DATE: 03-0CT-1988
ATLOND DATE: COMPATION:
APPLICATION NUMBER: US 07/415,029
FILING DATE: 25-SEP-1989
ATLONEY/AGENTINFORMATION:
ANAMOTE COMPATION:
ANAMOTE COMPATION:
ANAMOTE COMPATION ANAMOTE COMPATION:
ANAMOTE COMPATION ANA
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828 RGADYSLRAVRMKIRPLVTQ 847
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REGISTRATION NUMBER: 32,457
REFRENCE/DOCKET NUMBER: SCRO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 619-554-6312 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-373-157-4
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40.5%; Score 47; DB 4; Length 286;
Best Local Similarity 56.2%; Pred. No. 6;
Matches 9; Conservative 3; Mismatches 4; Indels
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                     ZIP: 94080
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winheatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,801
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DESGEY, GINGER R.
REGISTRATION NUMBER: 3,055
REFERENCE/DOCKET NUMBER: 91130P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEPHONE: 650/225-3216
TELEPHONE: 650/225-3216
TELEPHONE: 650/225-3216
TELEPHONE: 650/225-3216
TELEPHONE: GSO/952-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hillan, Kenneth
APPLICANT: Botstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Roy, Margaret
APPLICANT: Ferrara, Napoleone
APPLICANT: Tumas, Daniel
APPLICANT: 1130P3US
CURRENT APPLICATION NUMBER: US/09/202,088A
CURRENT FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: PCT/US98/19093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09202088A Patent No. 6551822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 KGSGYSLKATTMMIRP 283
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Gurney, Austin L.
Hillan, Kenneth
Botstein, David
Goddard, Audrey
Roy, Margaret
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Best Local Similarity 56.2
Matches 9; Conservative
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SEQ ID NO 20
LENGTH: 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: Linear
US-09-136-801-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: GODOWBK
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US-09-134-001C-4890
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US-09-202-088A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo
US-09-202-088A-20
       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94080
COMPUTER READABLE FORM:
MEDIUMER: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gurney, Austin
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Bostsein, David
APPLICANT: Goddard, Audrey
APPLICANT: Roy, Margaret
APPLICANT: Roy, Margaret
APPLICANT: Perrara, Napoleone
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: Tie Ligand Homologues
APPLICANT: Schwall, Ralph
TITLE OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Winbatin (Genorical)
SOFTWARE: Winbatin (Genorical)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,507
FILING DATE:
CLASSIFICATION: 536
ATTONES/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REGISTRATION NUMBER: 91130p1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                         US-08-960-507-20
; Sequence 20, Application US/08960507
; Patent No. 6057435
; GABERAL INFORMATION;
APPLICANT: Godowski, Paul J.
APPLICANT: GUANCY, Austin L.
TITLE OF INVENTION;
NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/09136801
Patent No. 6413770
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1|| ||: :| |||
268 KGSGYSLKATTMMIRP 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: Amino Acid
|||:||:|||||
1 YSMKKTTMKIIPF 13
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Best Local Similarity
Marches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-960-507-20
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: 1BM PC compatible

OFFRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/960,507

FILING DATE:

CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130p1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
                                                                                                                                                                                             APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 6, Application US/09136828; Patent No. 6350450; GENERAL INFORMATION:
                                                                                                                           ; Sequence 6, Application US/08960507; Patent No. 6057435; GENERAL INFORMATION:
                452 RGGAYSLRKAAMLIRP 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | ||:|| :| ||!
452 RGGAYSLRKAAMLIRP 467
                                                                                                                                                                                                                                                                                                                                                        CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KGSWYSMRKMSMKIRP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 470 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 56.2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   California
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US-09-136-828-6
                                                                                                          US-08-960-507-6
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                엄
Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNICE: GTC-007
CURRENT PAPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-10-10
RIOR FILING DATE: 1997-10-10
RIOR FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDLUM TYPE: 35 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/933,821 FILING DATE: CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: Dreger, Ginger R. REGISTRATION NUMBER: 91130 TELECOMMUNICATION INFORMATION: 750/952-3216 TELECOMMUNICATION INFORMATION: 750/952-3216 TELECOMMUNICATION SEQ.1981 INFORMATION: 650/952-3216 TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

40.5%; Score 47; DB 2;
Best Local Similarity 56.2%; Pred. No. 10;
Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Staphylococcus epidermidis US-09-134-001C-4890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-933-821-6

Sequence 6, Application US/08933821

Patent No. 5972338

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

TITLE OF INVENTION: The Ligands

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KGSWYSMRKMSMKIRP 16
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4 SFRRVTMKLKPFLP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 470 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-933-821-6
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US-09-132-928A-6

1 Sequence 6, Application US/09332928A

Patent No. 6368853

CANTORMATION:

APPLICANT: Godowski, Paul J.

ITILE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSES: Genentech, Inc.

STREET: 1 DNA WAY

CITY: South San Francisco
STREET: 1 DNA WAY

CITY: South San Francisco
STREET: 1 DNA WAY

COUNTRY: USA

IP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winbatin (Genentech)

CURRENT APPLICATION NUMBER: 09/9332, 928A

FILING DATE: AUTONO NUMBER: 08/9333, 821

REGISTRATION NUMBER: 08/933, 821

REGISTRATION NUMBER: 01130

TELEPONMUNICATION INFORMATION:

REGISTRATION NUMBER: PLI30

TELEPHONE: 650/952-3216

TELEPHONE: 650/952-3216
                                                                                                                                                                                                                                                                                                                                                          Query Match

40.5%; Score 47; DB 3; Length 470;
Best Local Similarity 56.2%; Pred. No. 10;
Matches 9; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
40.5%; Score 47; DB 3; Length 470;
Best Local Similarity 56.2%; Pred. No. 10;
Matches 9; Conservative 3; Mismatches 4; Indels
               FILING DATE:
CLASSIFICATION:
ATTORNEY, AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130R1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-3216
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-136-828-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-332-928A-6
APPLICATION NUMBER: US/09/136,828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| ||:|| :| ||:
452 RGGAYSLRKAAMLIRP 467
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